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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. 129 bp mRNA linear EST 14-AUG-2002 QGB21M16.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QGB21M16, mRNA sequence. BQB53899 Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca sativa. BQ853899.1 GI:22239364 Lactuca. (bases 1 to 129) akozik@atgc.org [michelmore@vegmail.ucdavis.edu]

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                               Submitted (17 JUN-2002) Weisshaar B., Max-Planck-Institut fuer Duechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F23H6. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
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Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
lanking sequence tag based reverse genetics
                                                                                                                                                                                                                       Rosso, M., Strizhov, N. and Weisshaar, B.
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TAG_LIB-QG_ABCDI lettuce salinas
TAG_TISSUE-chemical induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
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from 10 different sources of RNA from a single genotype.
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
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source
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http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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Arabidopsis thaliana T-DNA flanking
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Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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                      /strain="Columbia 0"
/db_xref="taxon:3702"
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/db_xref="taxon:3702"
/clone="GK-118B03-012518"
                                                                                /organism="Arabidopsis thaliana
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
The Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases 1 to 178)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Linang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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BH243164 199 bp I
AUIHC32TR AUIH Arabidopsis thaliana
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Tel: 301 838 0200
Fax: 301 838 0208
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For addtional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
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Arabidopsis thaliana
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                                                                                                                                                                                                                               /clone_lib="LERA"
/note="Organ: Leaf; Vector:
sheared to 0.9-1 Kbp before
a 26 c 30 g 73 t
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/db_xref="taxon:3702"
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Best Local :
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                                                                                                     Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                  Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 216)
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Arabidopsis thaliana genome survey sequence T7 end of BAC T3D23
TAMU library from strain Columbia of Arabidopsis thaliana, genom
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l Similarity 100.
18; Conservative
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AL089107
AL089107.1 GI:5290247
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Town, C.D., WhiteLaw, C.A., Pai, G., Van Aken, S.E:, Ut
Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC F1307
Unpublished (2001)
                                                                                                                                                               Genoscope.
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Fax: 301-838-0208
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9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
From Wash. U contig 1003.
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                                                                     www.genoscope.cns.fr)
Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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/note="Vector: pHOS2; Site_1:
DNA inserted into pHOS2 using
42 c 34 g 68 t
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                                                                                                                                                                                                                                   Brottier, P., Wincker, P.,
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KEYWORDS
SOURCE
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VERSION
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B62585/c
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AUTHORS
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BH243803
LOCUS
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ORGANISM
                                                               DEFINITION
                                                                                                                                                                                                                                                         BASE COUNT
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Best Local
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                                                                                                                                          136 TGGCGCCGTTGCCAATTG
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                                                                                                                                                                                            18;
                                                              T22F21TF TAMU
                                                                                                                                                       1 TGGCGCCGTTGCCAATTG 18
thale cress
                          B62585.1 GI:2629347
                                                                             B62585
                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Survey sequencing of Arabidopsis thaliana BAC F9022 Unpublished (2001) Other_GSSs: AUIRB17TF
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Town,C.D., Whitelaw,C.A., Pai,G., Van Aken,S.E., Utterback,T.V., Feldblyum,T.V. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AUIRB17TR AUIR Arabidopsis tl
                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Drive, 301-838-3523 301-838-0208
                                                                                                                                                                                           Conservative
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/clone_lib="TAMU"
/note="end : T7"
a 40 c 40 g
                                                                                                      FAON
                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/cione="AUIRB17"
                                                                                                                                                                                                                                                     /clone_lib="AUIR"
/note="Yector: pHOS; Site_1: BstXI; 2-3 kb sheared
/note="Yector: pHOS2 using BstXI linkers"
DNA inserted into pHOS2 using BstXI linkers"
45 c 48 g 109 t
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                                                             Arabidopsis
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                                                                                                                                                                                       Score 18; DB 17;
Pred. No. 1.1e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18;
Pred. No.
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s thaliana
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                                                           linear
clone T
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c clone
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                                                           r GSS 21-NOV-1997
T22F21, DNA
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AUIRB17, DNA
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RESULT 9
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Best Local :
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source
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                                                                                                                                                              Feldblyum,T.V. and Fraser,C.M.
Survey sequencing of Arabidopsis thaliana BAC
Unpublished (2001)
Other_GSSs: AUIWAS6TR
Contact: Chris Town
                                                                                                                                                                                                                                                                             Arabidopsis thaliana.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; Enassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
BH244138
                             Class: sheared ends
                                                           Email: cdtown@tigr.org
From Wash. U contig 1440
                                                                                               9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                    BH244138 401 bp 401 bp AUIWA26TF AUIW Arabidopsis thaliana
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                                                 From Wash. U contig
Seq primer: TF
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                         thale cress.
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Seq primer: M13-21
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Genomi
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update \bf 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 388)
Rounsley, S.D., Field, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                  (bases 1 to 401)
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                                               primer:
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                                                                                                                                                                                                                                               C.D., Whitelaw, C.A., Pai, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Location/Qualifiers
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/note="Vector: BeloBACII;
; Produced by Rod Wing"
71 c 77 g 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
| Strain="Columbia"
|/db_xref="taxon:3702"
|/clone="T22F21"
|/clone=lib="TAMU"
                                                                                                                                                                                                                                                                                                                                                                                       GI:16920790
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Pred. No. 1.3e+02;
; Mismatches 0;
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                                                                                                                                Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388
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c clone
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AUIWA26, DNA
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RESULT 11
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BH244101/c
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DEFINITION
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                                                                                                                                                               Query Match
Best Local S
Matches 18
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                                                                                                           302
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sequence.
BH243289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thale cress.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AUIHF63TR AUIH
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                     Class: sheared ends.
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From Wash. U contig 1440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.
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                                                                                                                                                             100.0%;
larity 100.0%;
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/strain="Columbia"
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="AUIWA26"
                                                                                                                                                                                                                              /clone_lib="AUIW"
/note="Vector: pHOS2; Site_1: BstXI; 2-3 kb sheared
DNA inserted into pHOS2 using BstXI linkers"
70 c 93 g 122 t
                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/clone="AUIWA38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"vector: pHOS2; Site_1:
DNA inserted into pHOS2 using
91 c 69 g 127 t
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            . .410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="AUIW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                      415 bp DNA linear GSS 13 Arabidopsis thaliana genomic clone AUIHF63,
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                                                                                                           285
                                                                                                                                                               0
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Pred.
                                                                                                                                                            Score 18; DB 17;
Pred. No. 1.3e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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s thaliana
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No.
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1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana BAC F13C23
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                                                                                                                                                                                       Length 410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear GSS 13-NOV-2001
clone AUIWA38, DNA
                                      GSS 13-NOV-2001
                                                                                                                                                               0,
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REFERENCE
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BH243156/c
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                                                                                                                                                                                                                                                                                     AUTHORS
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                  source
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BH243156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                            Unpublished (2001)
Other_GSSs: AUIHC93TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGGCGCCGTTGCCAATTG 18
                                                                                                                                           9712 Medical Center Drive, Tel: 301-838-3523
                                                                                                                                                                                                                                                                  Town.C.D., Whitelaw,C.A., Pai,G., Van Aken,S.E., Utterback,T.V., Feldblyum,T.V. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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AUIHC93TR AUIH Arabidopsis thaliana
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Town,C.D., Whitelaw,C.A., Pai,G., Van Aken,S.E., Utterback,T.V.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                   Email: cdtown@tigr.org
From Wash. U contig 1003
                                                                                                                                                                                                                                                 Survey sequencing of Arabidopsis thaliana BAC F1307
                                                                                                                                                                                                                                                                                                                                                                                                                                BH243156.1
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From Wash. U contig 1003
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                                                                                                                          Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                             thale cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris
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                                                                    primer: TR
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                                                    sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="AUIHF63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .415
                  Location/Qualifiers
1. .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="AUIH"
/note="Vector: pHOS2; Site_1:
/note="Vector: pHOS2; Site_1:
/note="Vector: pHOS2 using
DNA inserted into pHOS2 using
DNA 199 c 81 g 119 t
organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                GI:16918936
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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                                                                                                                                                            MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 415;
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VERSION
KEYWORDS
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BH252783
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Best Local
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209 TGGCGCCGTTGCCAATTG
                                                                         18;
                                1 TGGCGCCGTTGCCAATTG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 bp DNA linear GSS 28-NOV-200 SALK_013862 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_013862, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 419)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H.,
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,
,Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered
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                                                                                                                                                                    105
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ecker@salk.edu
                                                                                                                                                       /clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 99 c 69 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Columbia"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="AUTHC93"
/clone="Jib="AUTH"
/note="Vector: pHOS2; Site_1: BstXI; 2-3 kb sheared BAC
'DNA inserted into pHOS2 using BstXI linkers"
a 82 c 94 g 90 t
                                                                                                                                                                                                                                                                                                                               /strain="Columbia 0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                  /clone="SALK_013862"
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                                                                                         100.0%;
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226
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                                                               Score 18; DB 1/,
Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the left border of
                                                                                                    Length 419;
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                                                                   Indels
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Prednis, L., Shinn,
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                                                                 Gaps
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BH244079
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BH244105/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                    96 TGGCGCCGTTGCCAATTG
                                                                                Survey sequencing of Arabidopsis thaliana Unpublished (2001)
Other_GSSs: AUIRB53TF
                                                                                                                                                                                                                                                                                          sequence.
BH244079
                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                 Contact: Chris Town
                                                                                                                             1 (bases 1 to 424)
Town, C.D., Whitelaw, C.A., Pai,
Feldblyum, T.V. and Fraser, C.M.
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Survey sequencing of Arabidopsis thaliana BAC F13C23
Unpublished (2001)
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

June 20, 2003, 19:31:16 ; Search time 75.6226 Seconds (without alignments) 6927.165 Million cell updates/sec

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SUMMARIES

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                           Submitted (31-AUG-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org Address all correspondence to:at@tigr.org
                                                                                                      Submitted (09-AUG-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org 3 (bases 1 to 1843); Town,C.D. and Kaul,S.
                                                                                                                                                                                                                             Town,C.D., Haas,B.J., Wu,D., Maitl,R., Hannick,L.I., Chan,A.P., Tallon,L.J., Rooney,T., Utterback,T.R., Vanaken,S.E., Feldblyum,T.V., White,O. and Fraser,C.M.
Arabidopsis thaliana chromosome 3 BAC F1C23 genomic sequence upublished
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Submitted (16-OCT-2001) Hirokazu Kotani, Kazusa DNA Research
Institute, Lab. Chromosome Research II; 1532-3 Yana, Kisarazı
Chiba 292-0812, Japan (E-mail:kotani@kazusa.or.jp,
Tel:81-438-53-3920, Fax:81-438-52-3921)
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and annotation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named indicate the level of evidence for their annotation. Genes with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MCMAYLVVFRYFGCFWSSNRGKTEHEVRMPNDAFSKSTLSOPWS
PARGRWTIQSRHHYISLDRKTKPLKPSLINDILDHWKAHFSPLDANDTFGRRIMT"
a 3632 c 3666 g 5742 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(365. .405)
/rpt_family="AT_rich"
2852. .5536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAK96023.1"
/db_xref="GI:15383840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to protein prospero GI:1346808 (Drosophila
melanogaster)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(16226. .16384,16614.
/gene="F1C23.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<16225. .16384,16614.
/qene="F1C23.2"
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/gene="F1C23.2"
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/clone="F1C23"
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="3"
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                                                                                                                                                                      18813 bp
AC T9E19.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18433;
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                            Tracheophyta;
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Strowmatt,C., Johnson,D. and Le,T.
The sequence of A. thaliana T9E19
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 5' clone is T2L5, 200 bp overlap; 3' clone is F7N22, 200 bp overlap. Actual start of this clone could not be found, the first known base of overlap is at 36622 of T2L5; actual end is at 76001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       once,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-NOV-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neighboring submissions.
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                                                                                                                                                                                                                   /gene="T9E19.2"
join(57. .893,96
/gene="T9E19.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Genetics, wast. Louis, MO 63108, USA e-mail: rwilson@watson.wu
/evidence=not_experimental
/protein_id="AAC72876.1"
/protein_id="AAC72876.1"
/db_xref="G1:3859611"
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NVKPECESVMNTLFDERFGDTVPTIADLVSWLDEEESMEGWGQLALSLIILVDGVVAA
HSNPNRFTSKTVEMMKLKEFCKYPWGRVSFTRTLGRIANFQTPYDAQQLIRDLYGS
YALHGFPLALQLLAFETIPSIAKLGPDDVLNRFFAERSHRLASLBAIRTSRILECEA
ADEVEVNYIVKPADNVCPPSLSWDDEVDDPRVDYIEALLIDGHQWQEDEWVGGYARVP
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis
/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                  /map="5"
                                                                                                                                                                                                                                                                                                         /clone="T9E19"
                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                         /chromosome="IV"
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'9E19.2"
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-FEB-2002) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.or.*
* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is a rabitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Town,C.D., Haas,B., Tallon,L.J., Rooney,T., Ciecko,A., Utterback,T., Vanaken,S., Feldblyum,T., White,O. and Fraser,C.M. Arabidopsis thaliana 'IGF' BAC 'F9022' genomic sequence near marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC109921
AC109921.1 GI:18640653
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                            runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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n,C.D., White,O. and Fraser,C.M.
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APVTGKKPSTRUSTKGSTETRKSSRLTRVSHDVDTPALSFGCNSKEEDDLDPGVHTTA
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YYTOEERPVEEATVDTEMEEYPSNESARVSEVDLLDNGPKDVAEPGLVGTHTGADEIA
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GESKLVTGMEVEIPEKTHSDPPSPFQVVNNVIRELDTKAVGDLAAATDVEELRILTQG
QTHLLTKRVGDFKKCFNKNGFKWGKLLSDIANGVHINREPNMKWLKDVDVVYAPMNWK
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14290. .14391,14462. .14521,14645. .15124)
/gene="T9E19.1"
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/gene="T9E19.1"
  gap of unknown 1
9078: contig of 3046 b
9120: gap of unknown 1
11911: contig of 2791 by
11953: gap of unknown 1e
15042: contig of 3089 bo
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Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598734.
Location,Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-MAR-2000) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C., Fraser,C.M. and Venter,J.C.
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 33329)
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/strain-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"unknown"
/clone-"IGF-F9022"
a 6125 c 6878 g 939
                                                                  complement(383. .431)
/rpt_family="AT_rich"
complement(2109. .2135)
/rpt_family="AT_rich"
complement(311-126)
                                   complement(2211. .2267)
/rpt_family="AT_rich"
                                                                                                                                        /note="2721 nt before this point were not included in the submitted sequence, due to overlap with another BAC"
                                                                                                                                                                                                                      complement(1. .482)
rpt_family="AT_rich"
                                                                                                                                                                                                   /note="overlap with BAC clone F15K19 (AC006429:1. .482)."
                                                                                                                                                                                                                                            /map="g4532"
/clone="F16G22"
                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/cultivar="columbia"
/db_xref="taxon:3702"
/chromosome="2"
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                                                                                                                                                                                                                                                                                             /rpt_family="AT_rich"
complement(13763. .16746)
/gene="At2g10900"
/note="r*c"
                                                                                                                                                                                                              /note="F16G22.4; similar to GB:AAA75253; some members of this protein family have a weak CCHC zinc fingers that is mostly from retroviral gag proteins (nucleocapsid) complement(join<13763. .14997,15212. .15445,15881. .1608
     /translation="mmmvilchygrvigrvnddgegsystkgssgvykmgsrlldlyv
Ewwiecrgrviccrgcgqvlqelqddlllfdlkerssyvftviqgfdlsfvirnlfqt
RVVYHLEKGRSVGIIXDQaPGfrygfsekaqivigfgrgmsqsglvnqgsnvsntmkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="DNA sequence similar GB:U76697"
                                                          /product="putative Tall-like
/protein_id="AAD28647.1"
/db_xref="GI:4733964"
                                                                                                                                                                                                                                                                                                                                                                                                  complement(11206. .11773)
/gene="At2g10910".
/note="DNA sequence similar to non_LTR retrotransposon
psuedogene for reverse transcriptase GB:L47192"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNTEEVVAEMEEAVVITRDIAEVVVEKDTVVVAVREVAKEEVTL EATEETEWGLVIKDSLVLCHR" complement(7921...7948) /rpt_family="AT_rich"
                                                                                                                                                                           complement (join (13763.
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7271. .7442
                                                                                                                       codon_start=1
                                                                                                                                        'gene="At2g10900"
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/note="mirror"
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/protein_id="AAD28646.1"
/db_xref="GI:4733963"
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complement(6054. 6076)
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LVLVLYCVRVLMLDQYQETIALSQEVMMEDGRREFNVPMNCPIPVVKRRMKAPKHVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD28645.1"
/db_xref="GI:4733962"
/translation=""-"
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complement(3184. .3205)
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/rpt_family="AT_rich"
2951. .2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="At2g10920"
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/oin/5/77
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/gene="At2g10930"
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join(5423. .56
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22177. .
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retroelement.#Rf:ATR0033|X81801 Athila retroelement"
22416 . 22595
                                                                                                                                                                                                                                                                                                                                                            106B"
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Rf:106B centromeric repeat x93611, 106B is diverged copy of the Athila retroelement, 300 coples#Rf:gill100798|emblx93611.1|A7106B A.thaliana centromeric repeat region (clone 106B)#Rf:ATR0044|x93611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(24277. .24387)
/rpt_family="Rf:centromeric repeat from T7M24 17342 to
19092 1751nt includes within it 106B centromeric repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
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/db_xref="G1:473965"
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A.thaliana DNA of a 180bp satellite
junction#Rf:ATR0034|X89195 clone H12 of Athila 180-bp
                              complement(25459. .25710)
/gene="At2g10870"
                                                                                                                                                        /rpt_family="Rf:centromeric | 19092 | 1751nt includes within complement(25459. .25710) /gene="At2g10870" /note="F16G22.7; predicted by /note="F16G22.7; pred
                                                                                                                                                                                                                                                                                                                              complement(25075. .25134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="F16G22.6; similar to hypothetical protein
GB:AAC26673"
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retroelement.#Rf:ATR0033|X81801 Athila retroelement"
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A.thaliana DNA of a 180bp satellite
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retroelement.#Rf:ATR0033|X81801 Athila retroelement"
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22349. .22631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGFPDHEKKMLEAFLAPEAGKTVTDLGTLGANMEGILSGTMPSKVVRKKFFSGPEEVT
IQNKAENALELAEQHDLFSDDLSQLLAQSSPLEGDPSLQFMDTKMEDKKSSGVELTHE
DGEFFAANEENFDGDKLEVVLLPINTVSEMNVNMVSVSENVPNEQAHEEEMEGKSQGE
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MRCP1FGDKGKQS1FKEDPKRDNTLQRYKGAA1NGSVPGTSSGSTRAVFAEPSQGLTS
IDKKDAS1QDSYNRSKQ1SG1KAKKGRRNLFVAPVQASSSQMAVQVTKLSQLQTDTVG
                                                                                              complement(<25459. .>25710)
/gene="At2g10870"
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2 1751nt includes within it 106B centromeric
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                                                                                                                                                                                                                                                              repeat from T7M24 17342 to it 106B centromeric repear
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Arabidopsis thaliana
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Sequence 194 from Patent
AX059461
                                                                                                       Plant chromosome compositions and met Patent: WO 0055325-A 233 21-SEP-2000;
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                                                                     University of Chicago (US)
Location/Qualifiers
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
7401 c 7909 g 9799 t
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/db_xref="taxon:3702"
7544 c 7078 g 10298 t
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/protein id="AAD28649.1"
/db_xref="G1:4733966"
/translation="MEFDGGVLALPAVFVAESFVGVEALVSQRLRKRKGKRVRLEEEE
DDEPELGVDANNEEDCGYYGDEDCDAVEDIVGGGENDDN"
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ORIGIN
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AX059548
LOCUS
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Best Local S
Matches 18
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                                                                                                                                                                                      source
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                          7762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238
                                                                             18;
                                                                                                                                                                                          Preuss,D., Copenhaver,G. and Kelth,K.
Plant Chromosome compositions and methods
Patent: WO 0055325-A 212 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 39104)
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 212
AX059479
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                                                                                                                                                                                                                                                                                                                                   thale cress.
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Sequence
AX059548
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Plant chromosome compositions and methods
Patent: WO 0055325-A 281 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
                      TGGCGCCGTTGCCAATTG 7779
                                             TGGCGCCGTTGCCAATTG 18
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                                                                            Conservative
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llarity 100.0%;
Conservative (
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                                                                                                                                    /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
7680 c 7833 g 12033 t
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/db_xref="taxon:3702"
7622 c 7434 g 11646 t
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                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                    39104 bp
from Patent WO0055325
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Pred. No. 80;
0; Mismatches
                                                                                       Score 18;
Pred. No.
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; Mismatches
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WO0055325.
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              DEFINITION
ACCESSION
                                                    RESULT 12
AX059477/c
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AUTHORS
TITLE
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ORGANISM
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VERSION
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AX059497/c
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ORIGIN
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KEYWORDS
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DEFINITION
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AX059456/c
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TITLE
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Best Local
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AX059477 42
Sequence 210 from Patent
AX059477 GI:12311582
                                                                                                                                 1 TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 42112)
Preuss, D., Copenhaver, G. and Keith, K.
Plant Chromosome compositions and methods
Patent: WO 0055325-A 230 21-SEP-2000;
                                                                                                                                                            . Similarity
18; Conserv
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AX059497
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Location/Qualifiers
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Plant chromosome compositions and methods
Patent: WO 005535-A 189 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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1 (bases 1 to 40480)
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AX059456
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18; Conservative
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Conservative (
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230 from Patent WO0055325.
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/db_xref="taxon:3702"
8525 c 8423 g 12287 t
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/db_xref="taxon:3702"
7912 c 8765 g 11297 t 2
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from Patent WO0055325.
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Pred. No. 80;
0; Mismatches
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Pred. No.
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AX059459/c
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ORIGIN
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AX059452
Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 47840)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 47383)
Preuss D. (Crenhaver G. and Keith K.
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Location/Qualifiers
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Sequence 192 from Patent WO0055325.
AX059459
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Plant chromosome compositions and methods
Patent: WO 0055325-A 210 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; eurosida II; Brassicales; Brassicace
1 (bases 1 to 42208)
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TGGCGCCGTTGCCAATTG 35872
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                                                                                                                                    47840 bp
185 from Patent W00055325
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/db_xref="taxon:3702"
9919 c 9688 g 13496 t 71
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/db_xref="taxon:3702"
8859 c 8866 g 11961 t
                                                                                                         GI:12311557
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1 (bases 1 to 48128)

Preuss,D., Copenhaver,G. and Keith,K.

Plant chromosome compositions and methods
Patent: WO 0055325-A 202 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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ALIGNMENTS

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AAF22288 AAF22302

WPI; 2000-105586/09.

New nucleic acid molecules for imparting agronomically significant

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                   This oligonucleotide represents plant retroelement primer binding site A of the invention. The invention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the
                                                                                                                                                         Disclosure; Page 115; 118pp; English.
                                                                                                                                                                                                          New nucleic acid molecules for imparting characters to plants, especially soybean
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 C; 6 G;
     especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; |
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention provides molecular tools
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
     when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Þ
                                                                                                                                                                                                                     agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB
  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               į.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
retroelement carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                               primer binding
                                                 vectors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT 3
AAF22281/c
ID AAF22281 standard; DNA; 59590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                     01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                       The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                            Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells \cdot
  Sequence
                                   the construction of transgenic plant and animal cells selected proteins such as hormones, enzymes, interleuk
                                                                                                        Claim 102; Page 351-364; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at least 1 agronomically-significant characteristic. In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an agronomically-significant characteristic and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site,
                                                                                                                                                                                WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                          17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Centromere; michrosome; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC containing
                                                                                                                                                                                                                             (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                    18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                         WO200055325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF22281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNAse-H sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oviral particles that are plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 TGGCGCCGTTGCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
  59590
                       cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gag, integrase,
                                                                                                                                                                                                     Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
                                                                                                                                                                                                                                                                                                                           2000WO-US07392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 BP;
                                                                                                                                                                                                                                                                99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
                                                                                                                                                                                                                                                    9908-0154603
                                                                                                                                                                                                                                                                                                                                                                                                                                               repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39· A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see AAZ35254-61). Also provi
17614 A;
                      antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                        Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reverse transcriptase, protease or 35254-61). Also provided are plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ი;
12031 C; 13575
                                                                                                                                                                                                                                                                                                                                                                                                                                               centromeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                         ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                      growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Т;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
G;
                     factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                              #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                 interleukins,
16118 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                             expressing
252 other;
                                                                                                                                       , useful for
                                 clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Query Match Best Local Matches

Similarity

100.0%;

.08;

Conservative

0

Score 18; DB Pred. No. 12; Mismatches

DB 12;

21;

Length 59590;

0

0,

Gaps

0

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RESULT 5
AAF22283/c
ID AAF22283 S
XX
AC AAF22283;
XY
DT 20-MAR-200
XX
XX
E BAC contai
XX
Centromere
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AAF22279/c
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC
Centromere; michrosome; vector; ds.
                                                                    20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                 Sequence 64415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 102; Page 321-335; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF22279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF22279 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2000;
                                                                                                                                                                                                                          35451
                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35456
                                containing repeats from centromeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ď
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                                                                                                                                                                                                                                                                                           . Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV
                                                                                                                                                                                                                                                                                                                                                                                               cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGCCGTTGCCAATTG
                                                                                                                                      standard;
                                                                                                                                                                                                                        TGGCGCCGTTGCCAATTG 35434
                                                                                                                                                                                                                                                          TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCGCCGTTGCCAATTG 35439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         michrosome;
                                                                                                                                                                                                                                                                                           100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHICAGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US07392
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                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                                                                                                                                                                                             BP; 18698 A; 13554 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeats from centromeres
                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                      83390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keith
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                         Score 18; DB Pred. No. 12; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds
                                                                                                                                                                                                                                                                                                                                                             13083 G; 18980 T;
                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #2
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                         Length 64415;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as vectors for
                                                                                                                                                                                                                                                                                                                                                             100 other;
                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                         0
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                                              18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
            (UYCH-) UNIV
                                                                                                                                                    17-MAR-2000;
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Query Match
Best Local Similarity
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                               Claim 102; Page 386-404; 1449pp; English.
                                                                                                                                                                                                                                                                                                 Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors furthe construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                     Sequence 83390 BP;
                                                                                                                                                                                                                                                                                                                                                                                                            Preuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                         factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                                                                                                                                           2000-587529/55.
                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                            Ď
_
TGGCGCCGTTGCCAATTG 18
                                                                                                                                     cytokines, antibodies, and growth factors.
                                                                                                                                                         proteins such as hormones,
                                                                                                                                                                                                                                                                                                                                                                                                            Copenhaver
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2,000WO-US07392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0125219
                                                                                                     24664 A; 17305 C;
                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                            ú
                                                                                                                                                                                                                                                                                                                                                                                                              Keith
                               0;
                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            7
                                   Mismatches
                                                                                                                                                           enzymes,
                                                                                                     17224 G;
                                                                    DB
                                                                  21;
                                                                                                                                                       interleukins,
                                 0,
                                                                                                     24140 T; 57 other
                                                                  Length 83390;
                                   Indels
                                                                                                                                                       clotting
                               0;
                               Gaps
                               0
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RESULT 6
AAF22289/c
ID AAF22289 standard;
                                       BAC
Arabidopsis
                   Centromere;
                                                          20-MAR-2001
                                                                              AAF22289;
                                      containing
thaliana
                    michrosome;
                                                         (first
                                       repeats
                                                                                                DNA;
                                                         entry)
                                       from centromeres
                    vector;
                                                                                                90336
                    ds
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CHICAGO

2000WO-US07392

99US-0125219. 99US-0127409. 99US-0134770. 99US-0153584.

99US-0154603

71262 TGGCGCCGTTGCCAATTG 71245

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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22288/c
AAF22288 standard; DNA;
                                                                                                                                                                                                                             18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                           The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing
                                                                                          Claim 102;
                                                                                                           Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve as the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                   BAC
                                                                                                                                                                                                         (UYCH-)
                                                                                                                                                                                                                                                                                                 17-MAR-2000; 2000WO-US07392.
                                                                                                                                                                                                                                                                                                                          21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                            Centromere; michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF22288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selected proteins such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokines, antibodies, and growth factors.
                                                                                         Page
                                                                                                                                                                                   Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 529-549; 1449pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
llarity 100.0%;
Conservative (
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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         antibodies, and
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                   hormones,
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                     interleukins,
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RESULT 9 AAF22282/ ID AAF2

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ВP

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AAF22282; AAF22282 밁

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AAF22302/c
D AAF22302 standard; DNA; 94895
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromerre. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                                                                                             Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a the construction of transgenic plant and animal cells -
                                                                                 Sequence 94895 BP; 28943 A;
                                                                                                                                                                           Claim 102; Page 804-819; 1449pp; English.
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                   1 TGGCGCCGTTGCCAATTG
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99US-0134770.
99US-0153584.
99US-0154603.
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RESULT 10
AAF22297/c
ID AAF22297;
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AC AAF22297;
XX
DE BAC containing repeats from XX
Centromere; michrosome; vox
XX
Centromere; thaliana.
XX
Cos Arabidopsis thaliana.
XX
PM W0200055325-A2.
XX
PD 21-SEP-2000.
XX
XX
11-MAR-2000; 2000WO-US073
XX
PR 11-MAR-1999; 99US-01252
PR 01-APR-1999; 99US-01274
PR 18-MAY-1999; 99US-01274
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Best Local
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 102;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for
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18; Conserv
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                                                                                                                                                                                                                                                                                                           TGGCGCCGTTGCCAATTG 55819
                                                                                                                                                                                                                                                                                                                                                                                                         95223 BP; 27974 A; 19452 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copenhaver
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99US-0153584.
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
The present invention relates to a recombinant DNA construct (Arabidopsis thaliana) centromere. The constructs are useful
                                                          Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
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                                    Claim 102;
                                                                                                                                   Preuss
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17-SEP-1999;
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99US-0154603.
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RESULT 12
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                                                              Query Match
Best Local S
Matches 18
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                   The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                            Sequence 109973 BP;
                                                                                                                                                                                                                                                                 Claim 102; Page 738-763; 1449pp; English.
                                                                                                                                                                                                                                                                                             Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                              Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCH-) UNIV CHICAGO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Centromere; michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC containing repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF22298 standard; DNA; 109973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing stably inherited michrosomes which can serve as vectors for
the construction of transgenic plant and animal cells expressing
selected proteins such as hormones, enzymes, interleukins, clotting
factors, cytokines, antibodies, and growth factors.
                                                                                                                                                           ractors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 96988 BP; 29654 A; 18289 C; 18523 G; 30522 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49874
   5453
                                                                                                                                                                                                                                                                                                                                                               2000-587529/55
                                                               18;
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
TGGCGCCGTTGCCAATTG
                                                                                                                                                         cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCGCCGTTGCCAATTG 49891
                                                                                                                                                                                                                                                                                                                                                                                              Copenhaver G,
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                          31657 A; 23911 C;
                                                                                                                                                       antibodies, and growth factors.
                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from centromeres 1-4 #21
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   5470
                               18
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                                                                            Score 18;
Pred. No.
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Pred. No.
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                                                            Mismatches
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                                                                                                                            22655
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                                                                                           21;
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                                                                                                                          31745 T;
                                                                                           Length 109973;
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                                                              Indels
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                                                                                                                          5 other;
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                                                            Gaps
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RESULT

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Y PN X SX X X DE X T
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AAF22303/
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Best Local S
Matches 18
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                         AAF22303 standard;
                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve at the construction of transgenic plant and animal cells - \cdot
            WO200055325-A2
                                                                Centromere;
                                                                                          Arabidopsis
                                                                                                                    20-MAR-2001
                                                                                                                                               AAF22303;
                                                                                                                                                                                                                                                                                                                                                   Sequence 134499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 102; Page 453-484; 1449pp; English.
                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preuss D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAC containing repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2001
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                                                                                                                                                                                                                                         89656 TGGCGCCGTTGCCAATTG
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                                                                                                                                                                                                                                                                    1 TGGCGCCGTTGCCAATTG 18
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18; Conserv
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                                                                michrosome;
                                                                                          thaliana chromosome 2 centromere.
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                    (first entry)
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99US-0127409.
99US-0134770.
99US-0153584.
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                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                   41565 A;
                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                   42577 T;
                                                                                                                                                                                                                                                                                                                        Length 134499;
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                   2 other;
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0;

18-MAR-1999; 17-MAR-2000;

2000WO-US07392

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RESULT 15
AAF22305
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Best Local
                                                                                                                                                                                                                                               18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Centromere; michrosome; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF22305 standard; DNA; 1082138 BP
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                                                                                                       WPI; 2000-587529/55
                                                                                                                                                       Preuss
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                                                                                                                                                                                                    (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-2000; 2000WO-US07392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCH-) UNIV CHICAGO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 820-959; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copenhaver
                                                                                                                                                    Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana chromosome 4 centromere
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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99US-0127409.
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                                                                                                                                                    Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keith K;
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Pred. No. 13;
                                                                                                                                                    7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
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                                                                                                                                   Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
                                                                                                                                                                                                                                                                                      Claim 68; Page 977-1388; 1449pp; English.
                                                                                                                                                                    factors, cytokines, antibodies, and growth factors.
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                                 1 TGGCGCCGTTGCCAATTG 18
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Search completed: June 20, Job time: 13.3019 secs 2003, 21:58:19

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Copyright (c) 1993 - 2003 Compugen
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GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
APPLICANT: Voytas, Daniel F.
ITILE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: P-1065 ISURF Plant Retroelement CURRENT FILING DATE: 1999-05-28
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 150
TYPE: DNA
ORGANISM: Glycine max
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ery Match st Local tches 1	IT 1 9-322-478-1 9-322-478-1 9-322-478-1 quence 1, Application US/09322478 tent No. 6331662 NERAL INFORMATION. PPLICANT: Wright, David A. PPLICANT: Voytas, Daniel F. ITLE OF INVENTION: Plant Retroelements and Met URENT APPLICATION NUMBER: US/09/322,478 URRENT FILING DATE: 1999-05-28 ARLIER APPLICATION NUMBER: 60/087125 ARLIER FILING DATE: 1998-05-29 UMBER OF SEQ ID NOS: 41 OFTMARE: Patentin Ver. 2.0 O ID NO 1 LENGTH: 18 TYPE: DNA ORGANISM: Glycine max 9-322-478-1		86000000000000000000000000000000000000
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RESULT 3
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,727
FILLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130/206916
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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             APPLICANT:
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                          Local Similarity
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                                      INFORMATION:
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ROSEMAN, SAUL
BASSLER, BONNI
KEYHANI, NEMAT
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CHITLARU, EDITH
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Pred. No. 0.
                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
0.94;
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                                                                                                                                                                                                  Length 1713;
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              Query Match
Best Local Similarity
Watches 16; Conserve
                                                                                          ; NAME/KEY: CDS
; LOCATION: (225)..(1070)
US-09-053-702-1
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US-09-053-702-1
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                                                                                                                                                                                               SOFTWARE: PatentIn SEQ ID NO 1
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: YAMADA,
                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09053702 Patent No. 6229069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                  FILE REFERENCE: 230-122P
CURRENT APPLICATION NUMBER: US/09/053,702
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF
                                                                                                                                                ORGANISM: Mesembryanthemum crystallinum
                                                                                                                                                                     LENGTH: 1272
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 9203,
COMPUTER READABLE FORM:
"TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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NAME: Haile, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHITLARU, EI APPLICANT: ROWE, CHRIS APPLICANT: YU, CHARLES TITLE OF INVENTION: BACK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1713 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 13-FEB-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                591 GGCGCGGTTGCCAATTG 575
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16; Conserv
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1: CA
PRY: USA
TGGCGCCGTTGCCAATTG 18
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                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                         82.2%;
88.9%;
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                           Score 14.8; D
Pred. No. 56;
0; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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Best Local S
Matches 16
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SEQ ID NO 38
LENGTH: 3097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: U5/09/282,147
CURRENT FILING DATE: 1999-03-31
EARLIER APPLICATION NUMBER: U5/60/080,278
EARLIER FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS TITLE OF INVENTION: TRANSCRIPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: PCT/US97/12955 EARLIER FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VAKHARIA, V1kram
APPLICANT: YAO, Kun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 8288-9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PM PC compatible
COMPUTER: POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                FILING DATE: 0
CLASSIFICATION:
REGISTRATION NUMBER:
                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                  ADDRESSEE:
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16; Conserv
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                                                                                                                                                                                                                                  Washington
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Howardsk, Thomas S.
Vedvick, Thomas S.
Towardzik, Daniel R.
                                                                                                                                                                                                                                                               6300 Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09072596
                                                                                                                                                                                                                    USA
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Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                 Hendrickson, Ronald C.
ENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed,
                                                                                                                                                                                                                                                                                                                                                               odes, Michael J.
                                                                                                                                                                                                                                                                                    SEED and BERRY LLP
                 David J.
                                                                  05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Steven G.
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                                                                                 US/09/072,596
                                                                                                                                                                                                                                                                   Center,
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Pred. No. 6
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                                                                                                                                                                                                                                                                 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: Genomic DNA US-09-072-596-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08920812 Patent No. 5763188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                               TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 962 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Chicago
             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 29-AUC
                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                 FOPOLOGY:
                                                                                                                 ENGTH:
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15; Conservative
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                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Illinois
Clinical Isolate P2-2
                                                                                                              9515 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuhisa, Akio
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                                                               linear
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29-AUG-1997
                                                Genomic DNA
                                                                                 double
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93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                                                                             33,547
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Pred. No. 8
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Query Match

80.0%; Score 14.4;

DB 1;

Length 9515;

Gerstein, Murray & Borun South Wacker Drive

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RESULT 10
US-08-921-177-13/c
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US-08-920-827-13/c
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TELEFRA: 25-3856
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
TVPE: nucleic acid
TVPE: nucleic acid
                                  Patent No.
                                                 Sequence 13,
                                                                                                                                                                                      Matches
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                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                            MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                       3 GCGCCGTTGCCAATTG 18
                                                                                                                                                                                      l Similarity
15; Conserv
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                                   3, Application US/08921177 5798211
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      Ohno, Tsuneya
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Pred. No. 1.
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0; Mismatches
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US-08-362-577C-13/c
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US-08-921-177-13
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Best Local S
Matches 15
                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                         Sequence 13
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                      CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                       TITLE OF
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                COUNTRY: United States of America ZIP: 60606-6402
                                                               STATE:
                                                                            STREET: 6300 g
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/362,577 FILING DATE: 27-MAR-1995
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OPERATING SYSTEM:
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CITY: Chicago
                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
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INVENTION: Probe for Diagnosing Infectious Disease
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                                                           Illinois
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6300 Sears Tower, 233
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Uehara, Hirotsugu
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic DNA
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                                                                                                                                                                                                                 Tsuneya
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93.8%;
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Pred. No. 1
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                                                                                          Gerstein, Murray & Borun
South Wacker Drive
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Length 9515; Indels

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; STRAIN: Clinical Isolate P2-2
US-08-362-577C-13
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Best Local Similarity 93.8
5.5.00 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                     FILING LALL.
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
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                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 29-AUG-199
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Probe for Diagnosing Infectious Disease NUMBER OF SEQUENCES: 25
                                                              FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
               NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
                                                                                                                                                                                                                                                                                  COUNTRY: United States of America ZIP: 60606-6402
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515 GCGCCGTTGCCAATCG 500
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5. 5853998
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Matsuhisa, Akio
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29-AUG-1997
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93.8%;
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Pred. No. 1
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South Wacker Drive
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; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginc
; STRAIN: Clinical Isolate P2-2
US-08-920-828-13
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US-09-103-840A-2/c
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US-09-103-840A-2
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TITLE OF INVENTION: DNA SEQUENCES FOR TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/10 CURRENT FILING DATE: 198-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 2, Application US/09103840A Patent No. 6294328
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Patent No. 6294328
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRA.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                          APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
                                                                                                                                                                                                                                                                                                                                   1572527 TGCCGCCGTTGCCAAT 1572542
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TOPOLOGY: li
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l Similarity 93.8%;
15; Conservative
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93.8%;
                                                     US/09/103,840A
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Pred. No. 6
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Pred. No. 1.
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                                                                                                           FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
OGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
US-09-103-840A-1
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Search completed: June 20, 2003, 23:25:32 Job time : 12.1792 secs
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US-09-103-840A-1
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                            Query Match 80.0
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8%;
Matches 15; Conservative
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LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Obn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                              1572688 TGCCGCCGTTGCCAAT 1572703
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841864 TGGCGCCGTTGCCGAT 841849
                                                                                                                     1 TGGCGCCGTTGCCAAT 16
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93.8%; Pred. No. 67;
tive 0; Mismatches
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Pred. No. 67;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
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length: 2000000000
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18
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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'ogn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	18	100.0	18	10	US-09-965-553-1	Sequence 1, Appli
ν	18	100.0	150	10	US-09-965-553-36	36,
ი ა	15	83.3	412	9	US-10-101-464A-479	479,
4		82.2	266	10	US-09-878-574-15377	w
5 1	14.8	82.2	573	10	US-09-974-300-4705	
თ		82.2	861	9	US-09-938-842A-807	Sequence 807, App
		82.2	1089	10	US-09-974-300-764	~
ი 8		82.2	2155	9	US-10-002-050-11	Sequence 11, Appl
		82.2	2155	9	US-10-002-304-11	11,
		82.2	2155	12	US-10-003-152-11	e 11,
		82.2	2156	9	US-10-002-050-21	Sequence 21, Appl
c 12		82.2	2156	ø	US-10-002-304-21	Sequence 21, Appl
c 13		82.2	2156	12	US-10-003-152-21	21,
c 14	-	82.2	2284	9	US-10-002-050-13	>
c 15.		82.2	2284	9	US-10-002-304-13	13,
c 16		82.2	2284	12	US-10-003-152-13	Sequence 13, Appl
c 17		82.2	3097	ø	US-10-216-981A-2	, At
c 18	14.8	82.2	3293	9	US-10-149-819-25	
c 19	14.8	82.2	8095	9	US-09-989-920-73	-

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
13.4	13.8	&	&	&	œ	œ	œ	æ	œ	œ	œ	&	œ	œ	œ	&	œ	œ	&	&	14	14	14.4	14.4	14.4
74.4	76.7	7	7	7	7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	77.8	77.8	80.0	80.0	80.0
277	465237	13715	6378	6373	4588	3538	2940	1627	1405	1320	1078	897	897	897	576	538	538	476	365	174	3268	1392	1863	1854	943
10	10	7	9	9	9	9	10	12	Q	10	10	10	10	10	10	10	9	10	10	9	9	10	10	9	10
US-09-294-093B-2256	US-09-933-267A-1	US-08-781-986A-195	US-10-037-270-332	US-10-000-512-1	US-10-114-170-26	US-09-952-267-10	US-09-801-368-283	US-10-062-254-237	US-10-122-822-6	US-09-815-242-9819	US-09-974-300-2700	US-09-841-132-132	US-09-841-132-130	US-09-841-132-120	US-09-974-300-5436	US-09-925-299-369	US-09-925-299-369	US-09-974-300-5603	US-09-880-107-357	US-10-122-822-21	US-09-927-827-24	US-09-815-242-9820	US-09-815-242-9985	US-09-894-844-103	US-09-822-830A-533
Sequence 2256, Ap	Sequence 1, Appli	Sequence 195, App	Sequence 332, App	Sequence 1, Appli	Sequence 26, Appl	Sequence 10, Appl	Sequence 283, App	Sequence 237, App	Sequence 6, Appli	Sequence 9819, Ap	Sequence 2700, Ap	Sequence 132, App	Sequence 130, App	Sequence 120, App	Sequence 5436, Ap	Sequence 369, App	Sequence 369, App	Sequence 5603, Ap	Sequence 357, App	Sequence 21, Appl	Sequence 24, Appl	Sequence 9820, Ap	Sequence 9985, Ap	Sequence 103, App	Sequence 533, App

ALIGNMENTS

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RESULT 2
US-09-965-553-36
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; TYPE: DNA
; ORGANISM: Glycine max
US-09-965-553-1
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GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
                                                                                                                               Sequence 36, Application US/09965553 Patent No. US20020112259A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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                                                                                                                                                                                                                                                                               1 TGGCGCCGTTGCCAATTG 18
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-101-464A-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fas
SEQ ID NO 479
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 479, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 36
LENGTH: 150
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                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Nicowenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704.302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                  APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                INFORMATION
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                                                                                                                                                                                                                                                                                                                                                      3 GCGCCGTTGCCAATT 17
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                                                                                                                                                                                                                                                                                                              GCGCCGTTGCCAATT 18
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o. US20030046728A1
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                                                                                                                                                                                                         Application US/09878574
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                                                                                                                                                                                                                                                                                                                                                                                                              83.3%; Score 15; DB 9; 100.0%; Pred. No. 1e+02
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RESULT 6
US-09-938-842A-807
; Sequence 807, Application US/09938842A
; Patent No. US20020160378A1
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; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701070032H2
US-09-878-574-15377
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US-09-974-300-4705
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APPLICANT: Berka, R
APPLICANT: Clausen
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PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15377
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Best Local Similarity
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                                        APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/237,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR RETLING DATE: 2000-08-24
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                       APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379
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Zhu, Tong
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88.9%;
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Pred. No. 1.
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Pred. No. 1
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; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-764
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                SEQ ID NO 11
LENGTH: 2155
TYPE: DNA
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Best Local :
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                                                                                                                                                     APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                   PRIOR APPLICATION NUMBER: 60/140,584 PRIOR FILING DATE: 1999-06-23
                                                                                                                                   PRIOR APPLICATION NUMBER: 09/604,286 PRIOR FILING DATE: 2000-06-22
                                                                    SOFTWARE:
                                                                                    NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
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Local Similarity 88.98;
les 16; Conservation
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l Similarity 88.9%;
l6; Conservation
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                                                                PatentIn Ver.
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Vernet, Corine
Yang, Meijia
Boldog, Ferenc
Herrmann, John
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Pred. No. 1
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Pred. No. 1.4e+02;
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US-10-002-304-11
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                                         APPLICANT: Boldog, Férenc
APPLICANT: Herrmann, John
FILE REFERENCE: 15966-554 Cura-54 CON-S12
CURRENT APPLICATION NUMBER: US/10/003,152
CURRENT APPLICATION NUMBER: 09/604,286
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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Patent No. US20020151494A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herrmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CON-S8
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shimkets, Richard APPLICANT: Fernandes, Elma
         PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21
TYPE: DNA
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LOCATION: (16
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Vernet, Corine
Yang, Meijia
Boldog, Ferenc
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88.9%;
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Pred. No. 1.6e+02;
0; Mismatches 2;
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Pred. No. 1.
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; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-003-152-11
                                                                                                                                                                RESULT 12
US-10-002-304-21/c
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LENGTH: 2156
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                                                                                                              GENERAL INFORMATION:
                                                                                                                                 Sequence 21, Application US/10002304 Publication No. US20030036185A1
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Best Local Similarity
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                                                            APPLICANT: Shimkets, Richard APPLICANT: Fernandes, Elma APPLICANT: Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Herrmann, John
TITLE OF INVENTION: NO. US20030032095Alel Nucleic Acid Sequences Encoding Human
FILE REFERENCE: 15966-554 Cura-54 CON-514
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604/286
PRIOR FILING DATE: 2000-06-22
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SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA
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LOCATION: (166)..(2037)
NAME/REY: variation
LOCATION: (1)..(2156)
OTHER INFORMATION: N may be any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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INVENTION: Polynucleotides and polypeptides encoded thereby
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Similarity 88.9%;
                             Fernandes, Elma
Vernet, Corine
Yang, Meijia
Boldog, Ferenc
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Vernet, Corine
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Boldog, Ferenc
                 Herrmann,
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Pred. No. 1
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NAME/KEY: CDS; LOCATION: (166)..(2037); NAME/KEY: variation; LOCATION: (1)..(2156); OTHER INFORMATION: N may be any nucleotide US-10-003-152-21
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US-10-003-152-21/c
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CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
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LENGTH: 2156
                                                                             Query Match
Best Local
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SEQ ID NO 21
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Best Local
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
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TITLE OF INVENTION: No. US20020151494A1e1
FILE REFERENCE: 15966-554 Cura-54 CON-S12
CURRENT APPLICATION NUMBER: US/10/003,152
CURRENT FILING DATE: 2001-11-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                                    LENGTH: 2156
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (166)..(2037)
NAME/KEY: variation
LOCATION: (1)..(2156)
OTHER INFORMATION: N may be any nucleotide
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1298
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                              1 TGGCGCCGTTGCCAATTG
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TGGCGCCGATGCCAGTTG 1281
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Vernet, Corine
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88.9%;
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                                                               Score 14.8; D
Pred. No. 1.6e
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Pred. No. 1.6e+02;
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RESULT 15
US-10-002-304-13/c
US-10-002-304-13/c
; Sequence 13, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
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; LOCATION: (166)..(1953)
; NAME/KEY: variation
; LOCATION: (1)..(2284)
; OTHER INFORMATION: N may be any nucleotide US-10-002-050-13
; OTHER INFORMATION: N may be US-10-002-304-13
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Best Local Similarity
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TITLE OF INVENTION: NO. US20030032095A1el Nucleic Acid Sequences Encoding Human Semap
FILE REFERENCE: 15966-554 Cura-54 CON-S14
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
                                                                                                                                                                                                                                                                                   APPLICANT: Herrmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CON-S8
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
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                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/140,584 PRIOR FILING DATE: 1999-06-23
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                 NAME/KEY: variation LOCATION: (1)..(2284)
                                                                       NAME/KEY: CDS
LOCATION: (16
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: Fernandes, Elma
: Vernet, Corine
: Yang, Meijia
                                                                       (166)..(1953)
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Vernet, Corine
Vang, Meijia
Boldog, Ferenc
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Pred. No. 1
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Search completed: June 21, 2003, 00:34:38 Job time: 8.65094 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1 ttggaggctgggctcatata.....tcctaggccacaagatctca
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University, 2208 Molecular Biology Bldg., Ames, IA 50011,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Submitted (08-MAY-2001) Department of Zoology and Genetics, Id State University, 2208 Molecular Biology, Ames, IA 50011, USA
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Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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/variety="Williams"
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/db_xref="taxon:3847"
                                                                                                                                                                                                          /note="nonfunctional reverse transcriptase
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Voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zoology and Genetics,
State University, 2208 Molecular Biology, Ames, IA 50011, Us
Location/Qualifiers
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Wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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<1. .>762
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/db_xref="taxon:3847"
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/variety="L85"
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Wright, D.A. and Voytas, D.F.
Direct Submission
Submitted (14-SEP-1999) 200logy and
University, 2208 Molecular Biology
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/strain="L85"
/db_xref="taxon:3847"
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                                      /rpt_type=dispersed 2331. .4014 4017. .6900
                                                                                                   /note="polypurine tract"
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/rpt_family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="retrovirus-like"/pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat/family="pat
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Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phas
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phas
wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
                                                                                                                                              sequence.
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Wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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Direct Submission
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/product="AAL06417.1"
/protein_id="AAL06417.1"
/db_xref="GI:15724028"
/translation="VKEVLKLLEVGLIYPISDSAWVSPVLVVSKKEGMTVIRNEKND
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VVDFKDQEKNAFTCPFGVFAYERIPFGLCNAPTTFQMCMLAIFADIYEKSIEVFMDDF
SVFVPSLESCIKKLEMVLQRCVETNLYLNWEKCHFMVREGIVLGHKISTRGIEVDQTK
IDVIEKLPPPSNVKGIRSFLGQARFYRRFIKDFTKV"

150 c 181 g 203 t
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/variety="L85"
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/db_xref="taxon:3847"
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Pred. No. 1.5e-126;
0; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Structural Analysis of a Lotus japonicus Genc Features and Mapping of Sixty-six TAC clones Regions of the Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus DNA, clone_lib:LjT library clone:LjT16107.
Lotus japonicus
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyLedons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lotus japonicus genomic complete sequence.
AP004896
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                           GAACTGTCACTGGTTGGCGAATGTGTATICGACTATICGCAAGCTGAATGAAGCCACACGGA
                                                                                     TTCCAAAGAAAGGAGGCATGACTGTGATTACTAATGACAAGAATGAGCTGATTCCGACAA
                                                                                                    TTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACAC
                                                                                                                                             TAGAAGCAGGTATGATTTATCCTATTTCTGATAGTTCTTGGGTGAGTCCAGTGCAGGTAG
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29650
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                        /organism="Lotus japonicus"
/db_xref="taxon:34305"
/chromasome="5"
/clone="LjT16107"
/clone="LjT16107"
/clone=lib="LjT llbrary"
/note="TAC Clone:TM0040"
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Pred. No. 1.3e-103;
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 26
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Voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zoology ar
State University, 2208 Molecular Biology, Ames,
Location/Qualifiers
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wright,D.A. and Voytas,D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
21638318
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Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                       Similarity 74.:
45; Conservative
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TGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCCTTGGGTAAGCCCAGTACAGGTGG
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a 132 c
                                                                                                                                                                   /note="endogenous_virus: <1. .>762
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/variety="Hark"
                                                                                                                                                      /note="nonfunctional reverse
                                                                                                                                                                                               /isolate="Soybean5-1"
/db_xref="taxon:3847"
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                                                                     58.8%;
74.3%;
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Pred. No. 1e-1
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Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zool
State University, 2208 Molecular Biology,
Location/Qualifiers
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Shaull,S., Lin,S., Dixon,R.,
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Shaull,S., Lin,S., Dixon,R., May,G., Su Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-5n3
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The University Of Oklahoma
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Submitted (31-MAY-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Cook,D., Kim,D. and Roe,B.
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Wright, D.A. and Voytas, D.F.
Direct Submission
Submitted (14-SEP-1999) Zoology and Genetics,
University, 2208 Molecular Biology Bldg., Amee
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                                                                  AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGAGACTAACTTGGTACTG
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                                                                                                 GTGGAAAAATGCATCGAAGTTTTCATGGATGATTTCTCTATTTTTGGGCCCATCCTTTAAG
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            AATTGGGAGAAATTCCATTTCATGGTTCAAGAAGGAATAGTGCTGGGGCCATAAAATTTCA
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nilarity 73.5%;
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.11100. .11106
/note-"polypurine tract"
.11109. .12472
a 2455 c 2912 g 4043
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3335...12472
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/rpt_type=dispersed
3335. .7628
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8205. .9350
/gene="envelope-like"
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|strain="L85"
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D; Mismatches 159
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Glycine max.
Glycine max
Glycine max
Glycine max
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Elycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Embryophyta;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Voytas, D.F. and Wri
Direct Submission
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Wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-MAY-2001) Department of Zoology and Genetics, State University, 2208 Molecular Biology, Ames, IA 50011, U.
                                                                                                                                                                                                                   TAGAAGCAGACCTTATTTATCCCATTTCGGATAGTACATGGGTTAGCCCTGTGCAAGTTG
TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGGTTTTTGGACCCTCATTTGACA
                                                         GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGG
                                                                                                                                                                             AGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCG
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/note="nonfunctional reverse tran
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/db_xref="taxon:3847"
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/variety="Hark"
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Search o	DЬ	Qy	Db	Qy	DЪ
Search completed: June 20, 2003, 23:24:00 Job time : 2522.09 secs	565 ATTGGGAGAAATGCCATTTCATGGTTCAAGAAGGAATAGTGCTGGGGCATAAAATTTCA 623	542 ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGGCATAGTCCTAGGCCCACAAGATCTCA 600	505 GCTACTTATCAAACCTTGAAAGAGTATTACAGAGATGTGAAGAGTCTAATCTAGTTCTCA 564	482 GCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGA 541	445 TGGAAAAATGCATTGAACTTTTCATGGACGATTTCTCTATTTTTGGGCCATCTTTTGAAG 504
	GAATAGTGCTGGGGCATAAAATTTCA 623	GCATAGTCCTAGGCCACAAGATCTCA 600	GATGTGAAGAGTCTAATCTAGTTCTCA 564	GGTGCGAAGAGACTAACTTGGTACTGA 541	TCTCTATTTTTGGGCCATCTTTTGAAG 504

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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Plant generic retrosleme Soybean retroeleme Soybean retroeleme Soybean retroeleme Soybean retroeleme Soybean retroelement containing rep	AAZ35261 AAZ35273 AAZ35280 AAZ35271 AAZ35277 AAZ35277 AAZ35277 AAZ35276 AAZ35260	21 21 21 21 21 21	12286 4609 597 9829 12571 9139 9139 94895	100.0 95.2 94.7 88.7 87.2 57.6 52.3 51.3	571.2 568.2 532 523.2 523.2 345.6 313.8 307.8	0 98765232
Plant retroelement	AAZ35258		600	100.0	600	—
Description	Ħ		Query Query Match Length DB	Query	Score	Result

WPI; 2000-105586/09.

ALIGNMENTS

RESULT 1
AAZ35258
ID AAZ3 Glycine max. Arabidopsis thaliana. Pisum sativum. Retroelement; retrovirus; transgenic plant; gene transfer; soybean; pea; reverse transcriptase; Calypso; athila; cyclops; ss. AAZ35258 standard; Wright DA, Voytas DF; (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F. 29-MAY-1998; 28-MAY-1999; 28-MAY-1999; 02-DEC-1999. W09960842-A2 Plant retroelement generic reverse transcriptase gene. 27-MAR-2000 AAZ35258; (first entry) 98US-0087125. 99US-0087125. 99WO-US11858. DNA; 600 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provides molecular tools in the form of retroelements and retroelements and retroelements and retroelements and retroelements. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Celaimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNASe-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that are used to transfer the nucleic acids into plant cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence comprises a consensus of reverse transcriptase gene sequences identified in revirus-like element (retroelement) calyps of soybean (see AAZ35280), cyclops of pea (see AAZ35266) and athila of Arabidopsis thailana (see AAZ35264). The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1(e); Page 80; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
     541
                                                         481
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                                                                                                               421
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                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
Similarity
                                                   AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                          GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGAC
                                                                                                                                                             GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                                                                                                                                                                                                                                                                                            GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGGAATGACTTGATACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           вP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cid molecules for imparting plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>(</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 600; DB 21;
Pred. No. 6.5e-193;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600;
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                           600
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В

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GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA

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AAZ35261
                              Matches
                                           Query Match
Best Local
                                                                                                                 retroelement containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least I agronomically significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrate, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that are used to transfer the nucleic acids
                                                                                                                                                                                                                                                                              The present sequence comprises a generic plant retroelement obtained from retrovirus like elements (retroelements) calypso of soybean, cyclops of pea and athila of Arabidopsis thaliana. The invention provides molecular tools in the form of retroelements and
                                                                                 Sequence 12286 BP;
                                                                                                                                                                                                                                                                                                                                                 Claim 1(h); Page 84-88; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wright DA, Voytas DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9960842-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant generic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ35261 standard; DNA; 12286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soybean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retroelement;
                                                                                                           plant
                              600;
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32434.
TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pea;
                                                                                                           cells.
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retrovirus; transgenic plant; gene transfer; Calypso; athila; cyclops; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retroelement
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99US-0087125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 1482..6887
                                                                               3748 A; 2540 C;
                          100.0%; Score 600; DB 21; 100.0%; Pred. No. 3.5e-192; tive 0; Mismatches 0;
                                                                                 2767
                                                                               G;
                                                                                                                                                                                                                                                                                                                                                                                  agronomically significant
                                                                                 3231
                                                                               Ŧ;
                                                     Length 12286;
                            Indels
                                                                               0
                                                                               other;
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                          Gaps
 60
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RESULT 3
AAZ35273
ID AAZ3
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This is the nucleotide sequence of the Calypso 1-3 retroelement soybean. It was identified by screening of a soybean lambda
                                                                                                                                                                                                                                          Retroelement;
Calypso 1-3;
                                                                                                                                                                                                                                                                                                                             AAZ35273 standard;
                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                      Soybean retroelement Calypso 1-3
                                                                          WPI; 2000-105586/09
                                                                                          Wright DA, Voytas DF
                                                                                                                                        29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                      W09960842-A2
                                                                                                                                                                                                                                                                                        27-MAR-2000
                           Example 3; Page 102–104; 118pp; English.
                                                       New nucleic
                                                                                                                                                                    28-MAY-1999;
                                                                                                             (WRIG/) WRIGHT (VOYT/) VOYTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 4397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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                                             acid molecules for imparting to plants, especially soybean
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                          retrovirus; transgenic
soybean; ss.
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                                                                                                                                        98US-0087125
99US-0087125
                                                                                                                                                                   99WO-US11858
                                                                                                             F. Þ
                                                                                                                                                                                                                                                                                                                            DNA; 4609
                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                   plant;
                                                 agronomically significant
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                                                                                                                                                                                                                                                    transfer;
          of
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RESULT 4
AAZ35280
ID AAZ3
XX
AC AAZ3
XX
AC AAZ3

standard;

DNA; 597

ВP

AAZ35280; 27-MAR-2000

(first entry)

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Best Local Sim.
Matches 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see ANZ35254-61). Also provided are plant retroviral particles that particles are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and invention provides molecular tools in the form of retroelements and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4609 BP; 1420 A; 949 C; 1146 G; 1094 T; 0
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                           541
                                                                                               481
                                                                                                                                                                421
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                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                                                                                                                                                                                                                                                              GTTCCCAAGAAAGGTGGAATGACAGTGGTACAAAATGAGAGGAATGACTTGATACCAACA
                                                                                                                                                                                                                 GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
               AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA
                                                                                AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACACTAACTTGGTACTG
                                                                                                                                 GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGAC
                                                                                                                                                                GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCCTCATTTGAC
                                                                                                                                                                                                 GGGTTATGTAATGTACCAGCCACATTTCAGAGGTGCATGCTGACCATTTTTTTCAGACATG
                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGTTTGAGGAACCTAGAAATGGTACTTCAGAGGTGCGTAGAGACTAACTTGGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 571.2; DB 21;
Pred. No. 1.2e-182;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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1773
                                                                                               540
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Soybean retroelement calypso reverse transcriptase

gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the reverse transcriptase gene of cretrovirus-like element (retroelement) calpso of soybean. The cinvention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse H sequence (see AAZ3524-61). Also provided are plant retroviral particles that comprise a retrovirus protein encoded by a nucleic acid sequence encoding a plant retroviral envelope protein and a nucleic acid including e.g. the present sequence. These plant retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 579; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 115; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1998;
28-MAY-1999;
                                                                                      181
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                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcriptase gene;
                                                                                                                                                                                                                                                                                          GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAAGGAATGACTTGATACCAACA 120
                                                                                                                                                                                                                                                                                                                                                                            TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
GTTCCCAAGAAAGGTGGAATGACAGTGGTACAAAATGAGAGGAATGACTTGATACCAACA
                                                                                                                                                                                                                                                                                                                                                     TTGGAGGTTGGGCTCATATACCCCCATCTCTGACAACGCTTGGGTAAGCCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voytas DF
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retrovirus; transgenic criptase gene; calypso;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ם ם
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99US-0087125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 121 C; 158 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 568.2;
Pred. No. 4e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                         .2; DB 21; Lengtl
4e-182;
ches 18; Indels
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This is the nucleotide sequence of the Calypso 1-1 retroelement of complete soybean. It was identified by screening of a soybean lambda complete soybean using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 complete soybean complet
                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules for imparting agronomically characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retroelement; retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ35271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ35271 standard; DNA; 9829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calypso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WRIG/) WRIGHT D
(VOYT/) VOYTAS D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTGGGAAAAGTGTCATTTTATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                   Page 95-98; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Voytas DF;
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99US-0087125
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                                                                                                                                                      Glycine max
                                                                                                                                                                                                     Retroelement;
Calypso 1-2; s
                                                                                                                                                                                                                                                                                                                               27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                  AAZ35272
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ35272 standard;
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     28-MAY-1999;
                                                   02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCCTAAGAAAGGCGGAATGACAGTGGTACGAAATGAGAAGGAATGACTTGATACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAGGCTGGGTTCATATACCCCCATCTCTGATAGCGCTTGGGTAAGTCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAGAAGAGCATCGAGGTATTTATGGACGACTTCTGGATTTTTGGACCCTCATTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                  soybean;
                                                                                                                                                                                                  retrovirus; transgenic soybean; ss.
  99WO-US11858
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.7%;
94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 12571
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Pred. No. 3.7e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                            plant; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see ANZ35254-61) Also provided are plant retroviral particles that
                                                                                                                                                                                                                                                                          soybean. It was identified by screening of a soybean lambda library using a reverse transcriptes probe. 2 Groups of soybea retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements invention provides molecular tools in the form of retroelements.
                                                                                                                                                                                             retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1998;
28-MAY-1999;
  Sequence 12571 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                       This is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wright DA, Voytas DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WRIG/) WRIGHT (VOYT/) VOYTAS
                                       particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Page 98-102; 118pp; English
                                     are used
                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ם ם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0087125.
99US-0087125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਸ ⊅
  3801 A;
                                         to transfer the nucleic acids
2382 C;
  2707 G; 3681 T;
                                                                                                                                                                                                                                                                                                                                                                                                                       Calypso 1-2 retroelement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agronomically significant
                                         into plant cells.
  0 other
                                                                                                                                                                                                                                                                                                                                                             and 1-3
                                                                                                                                                                                                                                                                                and
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Query Match 87.2%; Score 523.2; DB 21; Length 12571; Best Local Similarity 93.2%; Pred. No. 4.1e-166; Matches 559; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

421	361 4655	301 4595	241 4535	181 4475	121 4415	61 4355	1 4295	
GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGAC	GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG	CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC	TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT	AAGGACCATTTCCCCTTACCTTTCATGGATCAGATGCTGGAGAGACTTGCAGGGCAGGCA	CGAACTGTCACTGGTTGGCGAATGTGTATCGACTATCGCAAGCTGAATGAA	GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA	TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG	
480	420 4714	360 4654	300 4594	240 4534	180 4474	120 · 4414	60 4354	

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ARESULT 7
ARAZ352LT 7
ARAZ352LT 7
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ARAZ352LT 
  Query Match
Best Local Similarity
Matches 441; Conserv
                                                                                                                                                              which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see ARZ35254-61). Also provided are plant retroviral particles that
                                                                                                                                                                                                                                                                                                                                 retroelement containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line than the retroelement carries at least 1 agronomically-significant characteristic (ACS).
                                                                                                                                                                                                                                                                                                                                                                                                                            soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe 2 Groups of soybean retroelements were identified 1.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and primer binding site invention provides molecular tools in the form of retroelements are invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1998;
28-MAY-1999;
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calypso 2-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retroelement; retrovirus; transgenic plant; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean retroelement Calypso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2000
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                                                                                                                                               particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 104-107; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WRIG/) WRIGHT D
(VOYT/) VOYTAS D
                                                                                                9139 BP;
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                                                                                                                                          are used to transfer the nucleic acids into plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Voytas DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence of the Calypso 2-1 retroelement of
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean; ss.
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99US-0087125
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                                                                                             2835 A; 1599 C; 2010 G;
                      57.6%;
73.5%;
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  Score 345.6;
Pred. No. 6.2e
0; Mismatches
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                           .2e-106;
                                                                                                2695 T;
                                                 DB 21;
                                                                                                0 other
Indels
                                              Length 9139;
  0,
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  Gaps
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                        WPI; 2000-105586/09
                                                                       Wright DA, Voytas DF
                                                                                                                    (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                           29-MAY-1998;
28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pea retroelement cyclops reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retrovirus-like element (retroelement) cyclops of pea. The invention provides molecular tools in the form of retroelements and
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                                  AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATC
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                   AATTGGTAGAAGTGCCACTTCATGGTGACCGAGGGGATAGTGCTTGGCCATAAAGTC
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Pred. No. 8.4e-96;
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17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector the construction of transgenic plant and animal cells
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    CAAGAAAAAACCACTTTCACTTGTCCTTATGGGACCTTTGCTTACAAGCGTATGCCTTTC
                                                                        CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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                                                                                                                                                                               Best
                                                                                                                                                                                                      Query Match
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                         The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                              Sequence 1082138 BP; 348775 A; 194404 C; 195515 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells
                                                               1047007
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GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA
                                             TTAGATGTTGGGGTTATCTACCCTATCTCTGATAGCACTTGGGTATCTCCAGTTCATTGC 1047066
                                                                              TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                 proteins such as hormones, cytokines, antibodies, and
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                                                                                                                                                        Conservative
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                                                                                                                              uch as hormones, enzymes, interleukins, antibodies, and growth factors.
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                                                                                                                                                     Mismatches
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  The present
                        Claim 36(a); Page 112-113; 118pp;
                                                                                                                                    (WRIG/)
(VOYT/)
                                                New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                      WPI; 2000-105586/09
                                                                                                             Wright DA, . Voytas DF;
                                                                                                                                                                          29-MAY-1998;
28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                     Retroelement; retrovirus; transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, rever transcriptase, protease or RNAse-H sequence (see AA235254-61). A provided are plant retroviral particles that comprise a retroviru protein encoded by a nucleic acid sequence encoding a plant retroviral envelope protein and a nucleic acid including e.g. the present sequence. These plant retroviral particles are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and intermetical control control carries and secondary construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS) in a preferred method, a helper cell line which expresses gag, po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retrovirus-like element (retroelement) athila of soybean. Athila was identified in a BLAST search of DNA sequences generated by the control of the sequence of the relation of the sequence of the relation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                   CATGTTTGTTGAATCTTGGCAGGGTATTGACTAGGTGCGAAGAGACGCGAATCTTGTTCTCA
                                                                                                                                                                                                                                          TCGAGGAGATGTGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCTCTTTCTCCT
                                                                                                                                                                                                                                                                                                    TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACA
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RESULT 12 AAF22281/c ID AAF22281: XX AC AAF22281;

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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a pla (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 102; Page 351-364; 1449pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for
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                                                  AAGAAAAACCACTTTCACATGTCCCTACGGAACTTTTGCTTATAAGAGAATGTCATTTG
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GTTTATGTAATGCTCCTGCAACATTTCAGAGGTGTATGACCTCTATATTTTCAGATTTAA
               GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGG
                                                                                                                                                                                                               GAACTATAACTGGTCATAGAATGTGCATTGATTATAGGAAGTTAAATGCTGCATCTAGGA
                                                                                                                                                                                                                                        TCCCTAAAAAAGGGTGGAATGACTGTTGTCAAAAATGAAAAAGATGAACTAATCCCTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                              59590 BP; 17614 A;
                                                                                                                                                             AAGATCATTTTCCTTTACCATTCATTGACCAAATGCTTGAACGTTTAGCTAATCATCCAT
                                                                                                                                                                                    TTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACAC
                                                                                                        ACTATTGCTTTCTTGATGGATATAGTGGTTTCTTTCAAATACCAATTCACCCTAATGATC
                                                                                                                              ACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGATC
                                                                             AGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCG
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99US-0134770.
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69.3%;
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RESULT 13
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                         Sequence 83390 BP;
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
 The present invention (Arabidopsis thaliana)
                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f} the construction of transgenic plant and animal cells -
                                    Claim
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the construction of transgenic plant and animal cells expressing
selected proteins such as hormones, enzymes, interleukins, clotting
factors, cytokines, antibodies, and growth factors.
18-MAR-1999;
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99US-0125219
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                                                                                                                                                                                                                                                                                                                                                                      entry)
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Pred. No. 6.3e-91;
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plan (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve as the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 102; Page 804-819; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factors,
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CATGTTTGTTGAGTCTTGGCAGGTTATTGAGCAGGTGTGAGGAGACGAATCTTGTTCTCA
                                                                            GCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGGTGCGAAGAGAGACTAACTTGGTACTGA 541
                                                                                                                                     TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGACA 481
                                                                                                                                                                                   GTTTATGCAATGCTCCTGCAACATTTCAGAGGTGTATGACCTCTATATTTTCAAATTAAC 46285
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                                                                                                                       TCGAGGAGATGGTGGAGGTCTTCAAGGACGATTTTTTGGTCTATGGCCCCCTCTTTTTCCT
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99US-0154603.
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Pred. No. 6.5e-91;
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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301 CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC 360	241 TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT 300	241 TACTACTGTTTCTTGGATGGATACTCGGGGATACAACCAGATCGCGGTAGACCCCAGAGAT 300	181 AAGGACCATTTCCCCTTACCTTTCATGGATCAGATGCTGGAGAGACTTGCAGGGCAGGCA	181 AAGGACCATTTCCCCCTTACCTTTCATGGATCAGGATGCTGGAGAGACTTGCAGGGCAGGCA	121 CGAACTGTCACTGGTTGGCGAATGTGTATCGACTATCGCAAGCTGAATGAA	121 CGAACTGTCACTGGTTGGCGAATGTGTATCGACTATCGCAAGCTGAATGAA	61 GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120	61 GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACA 120	1 TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG 60	1 TIGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG 60	Query Match 100.0%; Score 600; DB 4; Length 600; Best Local Similarity 100.0%; Pred. No. 6.4e-199; Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; OTHER INFORMATION: Description of Artificial Sequence: plant ; OTHER INFORMATION: retroelement sequence us-09-322-478-11	ORGANISM: Artificial Sequence FEATURE:	TYPE: DNA	SEQ ID NO 11	NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0	EARLIER FILING DATE: 1998-05-29	EARLIER APPLICATION NUMBER: 60/087125	CURRENT APPLICATION NUMBER: US/09/322,478	FILE REFERENCE: P-1065 ISURF Plant Retroelement	CR TAYROUTION: Dist Botton Smooth and Wothods Bolated	APPLICANT: Wright, David A.	GENERAL INFORMATION:	Sequence 11, Application US/09322478	US-US-3/4/0-11

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APPLICANT: Wright, David A.

APPLICANT: Wright, David F.

TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/0871125

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; OTHER INFORMATION: retroelement sequence
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GENERAL INFORMATION:
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Best Local Similarity
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                      GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                                                                     CAGGAGAAGACGGCCTTTACATGCCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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Pred. No. 3.8e-198;
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; TYPE: DNA
; ORGANISM: Glycine
US-09-322-478-21
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US-09-322-478-21
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SEQ ID NO 21
LENGTH: 4609
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APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
NUMBER OF SEQ ID NOS: 41
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                                                                 GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCCTCATTTGAC
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Matches 579
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LENGTH: 597
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CURRENT FILING DATE: 1999-05-28
EARLIER REPLICATION NUMBER: 60/087125
EARLIER REPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wright, David PAPPLICANT: Voytas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Glycine
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                                                                                                                                                              GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
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97.0%;
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Pred. No. 7.5e-188;
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GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wrytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DAYE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 9829
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; ORGANISM: Glycine
US-09-322-478-19
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AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                      GTGGAGAAGAGCATCGAGGTATTTATGGACGACTTCTGGATTTTTTGGACCCTCATTTGAC
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Pred. No. 1.5e-174;
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US-09-322-478-20

Sequence 20, Appl Patent No. 633166 GENERAL INFORMATION

Application

US/09322478

APPLICANT: Wright,

David

INFORMATION:

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TITLE OF INVENTION: Plant Retroelements and Methods Rel FILE REFERENCE: P-1065 ISURF Plant Retroelement CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 12571
TYPE: DNA
ORGANISM: Glycine max
US-09-322-478-20
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                                                                                                                   Sequence 22, Application US/09322478 Patent No. 6331662 GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISUBE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
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Best Local Similarity
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93.2%;
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Pred. No. 2.1e
0; Mismatches
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APPLICANT: Wright, David A.

APPLICANT: Woytas, Daniel F.

ITITLE OF INVENTION: Plant Retroelements and Methods Rel

FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087125

EARLIER APPLICATION NUMBER: 60/087125

PARLIER FILING DATE: 1998-05-29

NUMBER OF 5EQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 597
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; ORGANISM: Pisum US-09-322-478-29
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US-09-322-478-29
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Patent No. 6331662
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LENGTH:
                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local
                             TYPE: DNA
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73.5%;
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Pred. No. 1.1e-109;
0; Mismatches 159;
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Match

Length

597;

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RESULT 9
US-09-322-478-27
; Sequence 27, Application
; Patent No. 6331662
; GENERAL INFORMATION:
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Best Local
Matches 42
                                                                                     SEQ ID NO 27
LENGTH: 600
TYPE: DNA
ORGANISM: Arabidopsis thaliana
S-09-322-478-27
                                                                                                                                                           APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods |
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                    SOFTWARE: PatentIn Ver.
                                      Local Similarity
nes 415; Conserv
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 52.3%;
70.4%;
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                                                 Score 304.6; DB 4;
Pred. No. 4.1e-96;
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                                     Mismatches 184;
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TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACA 481
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                                  ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA 600
                                                                            CATGTTTGTTGAATCTTGGCAĞGGTATTGACTAGGTGCGAAGAGACGAATCTTGTTCTCA
                                                                                                                 GCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGA 541
                                                                                                                                                       TCGAGGAGATGGTGGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCTCTTTCTCCT
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; LENGTH: 10482
; TYPE: DNA
; ORGANISM: Glycine
US-09-322-478-23
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                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: POSEQ ID NO 23
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISURE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                           Local
                                         4064 TGACAGTCATTAAAAATGATAAAGATGAATTAATATCCACAAGGACTGTCACCGGGTGGA
140
                                                                                                                                                                        20
                                                                                                                                                                                                                                           Similarity
                                                                TGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACACGAACTGTCACTGGTTGGC
GAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCCTTAC
                                                                                                                                                   ACCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTGGTTCCCCAAGAAAGGTGGAA
                                                                                                                              ACCCCATCTCAGATAGTGCGTGGGTTAGCCCGGTGCAGGTTGTTCTCAAGAAGGGAGGTA
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                      28.7%;
75.2%;
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Pred. No. 2.3e-49;
Pred. No. 2.3e-49;
                                                                                                                                                                                                                                                           Length 10482,
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US-08-855-449-2
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US-08-855-449-2/c
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Best Local !
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                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 22202
                                                                                                                                                  Local Similarity
les 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCLABALLAND, STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 13-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     1051
                                                                                   1111 CAAATGTGCGTCGATTACAGATATCTTAACACGACTAGCCCTAAAGACGATTTTCCACTG 1052
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GGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAGAAGACGGCCTTT 318
                            CCACTCATCGACATTCTGGTCGACAACACAGCCAATTATGCCTTACTCTCTTTTATGAAC
                                                     CGAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCTTA 198
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                                                                                                                                                  Conservative
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14-MAY-1996
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                                                                                                                                                           Score 69; DB 2;
Pred. No. 6.6e-14;
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                                                                                                                                               Mismatches 155;
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                                                                Matches
                                                                                           Query Match
                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7568 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694.
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          NAME: Woessner, Warren REGISTRATION NUMBER: 30
                                                             Local Similarity es 213; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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5482 GACTGGTTTTCAATTACAAGAGGCTAAATGACAACACATGGCCGGATCAATATTCATTGC
                 140 GAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCTTAC
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Somers, D. A.
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O. Box 2938
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                                                         Score 55.4; DB 2;
Pred. No. 9.8e-09;
); Mismatches 241
                                                                                        Length 7568;
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APPLICANT: Tzafrir, I.
APPLICANT: Somers, D.A.
APPLICANT: Somers, D.A.
APPLICANT: Lockhart, B.
APPLICANT: Lockhart, B.
APPLICANT: Torbert, K.
TITLE OF INVENTION: Sugarcane bacilliform virus profile Reference: 600.369US2
CURRENT APPLICATION NUMBER: US/09/349,546
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: US 08/694,869
EARLIER FILING DATE: 1996-08-09
EARLIER APPLICATION NUMBER: PCT/IB97/01338
EARLIER FILING DATE: 1997-08-13
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US-09-349-546-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 7568
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Wir
                                                                                                                                                                                                                                                                                                  Local Similarity 46.68; nes 213; Conservation
                                                            5602 TGAAGAGCGGGTTTCATCAAGTCGCCATGGATGAAGAAAGTATTCCATTAACAGCATTTT
                         320
CATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTATGTAATGCACCAG
                                                                                                                                                                  GACTGGTTTTCAATTACAAGAGGCTAAATGACAACACATGGCCGGATCAATATTCATTGC
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                                                                                                    GATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGATCAGGAGAAGACGGCCTTTA
                                                                                                                                           CCGGAATCAATGCTCTACTAAAAAATGTTGCAAGAGCAAAGATCTTCTCAAAGTTTGATT
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Pred. No. 9.8e-09;
0; Mismatches 241;
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TITLE OF INVENTION: Bs2 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                  RESULT 15
US-09-592-054-5
; Sequence 5, Application US/09592054
; Patent No. 6440684
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US-09-360-186-1/c
  GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Caps
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                                                                                                                                                                                                                                                              GCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGGTGGAGAAAAGCATCGAG
                                                                                                                                                                                                                                                                                                        CGAACCCGATATGGTCACTACAAATTTTTAGTCATGTCCTTCGGGTTGAGTAACGCCCCT
                                                                                                                                                                                                                                                                                                                                            ACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTATGTAATGCACCA
                                                                                                                                                                                                                                                                                                                                                                                     CTTCGTTCGGGTTACCATCAGTTGAAAATTAGGGAGTCAGACATACCCAAGACAGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                           GGATACTCGGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAGAAGACGGCCTTT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTAGGATTGATGACCTTTTTGACCAGCTTCAGGGTGCTAAGTGCTTTTCAAAAATAGAC
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46.8%;
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Pred. No. 5.3e-06;
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                                                                                                                                           23981
                                                                                                                                                                                 465
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378

24128

24068

258

24248

0

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APPLICANT: Beraud, Christophe
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
CURRENT ENERGY: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1421
TYPE: DNA
ORGANISM: Human
US-09-592-054-5
                                                                                                                            80
Search completed: June 20, 2003, 23:25:48 Job time: 76.6415 secs
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Best Local Similarity 51.7%;
Matches 77; Conservative
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                                                                                       604 CGGCTATGAACTCCCAGTCGTCCCGATCT 632
                                                                                                            173 CCACACGGAAGGACCATTTCCCCCTTACCT 201
                                                                                                                                                                                                 544 TIGCCTIGGATACIGITITCCTGTTIGGAACAGGGCAACAACICTAGGACIGIGGCCTCCA 603
                                                                                                                                                                                                                                                                                     53 TACAGGTGGTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAGGAATGACTTGA 112
                                                                                                                                                                                                                                                                                                                                                 ; Score 33.8; DB 4; Length 1421; pred. No. 0.12; 0; Mismatches 72; Indels 0
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Minimum
Maximum
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Perfect score:
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      Score
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
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      0 US-09-965-553-11

0 US-09-965-553-27

0 US-09-965-553-34

0 US-09-965-553-19

0 US-09-965-553-29

0 US-09-965-553-16

0 US-09-97-672-2

0 US-09-986-4-880-1

0 US-10-184-644-152
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3971.420 Million cell updates/sec
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Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 1871, App
Sequence 152, App
Sequence 152, App
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US-09-993-292A-1	US-10-184-634-138	US-10-184-644-138	US-09-918-995-33903	US-10-205-428-181	US-09-764-891-2253	US-09-732-224-6	US-09-732-224-3	US-10-184-634-346	US-10-184-644-346	US-09-925-300-825	US-10-175-523-110	US-09-918-995-8924	US-09-960-352-2591	US-09-960-352-10425	US-09-960-352-9011	US-09-960-352-12818	US-09-960-352-9257	US-09-822-827-438	US-09-780-669-438	US-09-759-143-438	US-10-010-940-438	US-09-895-814-438	US-09-895-793-438	US-10-012-896-438	US-10-021-577-1
Sequence 1, Appli	Sequence 138, App	Sequence 138, App	Sequence 33903, A	Sequence 181, App	Sequence 2253, Ap	Sequence 6, Appli	Sequence 3, Appli	Sequence 346, App	Sequence 346, App	Sequence 825, App	Sequence 110, App	•	Sequence 2591, Ap	Sequence 10425, A	Sequence 9011, Ap	Sequence 12818, A	Sequence 9257, Ap		Sequence 438, App	Sequence 438, App	Seguence 438, App	Sequence 438, App	Sequence 438, App	Sequence 438, App	Sequence 1, Appli

₽ QY QΨ 밁 δÃ OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: retroelement sequence US-09-965-553-11 US-09-965-553-11 PRIOR APPLICATION NUMBER: 60/087125 PRIOR FILING DATE: 1998-05-29 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 11 GENERAL INFORMATION: APPLICANT: Wright, David A. APPLICANT: Wright, David A. APPLICANT: Voytas, Daniel F. TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: P-1065 ISURF Plant Retroelement CURRENT APPLICATION NUMBER: US/99/965,553 CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: 09/322.478 PRIOR FILING DATE: 1999-05-28 PRIOR FILING DATE: 1999-05-28 Query Match Best Local Similarity Matches 600; Conserv Sequence 11, Application US/09965553 Patent No. US20020112259A1 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: LENGTH: 600 121 121 61 61 1 TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG 60 GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120 TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG 100.0%; ilarity 100.0%; Conservative 0 0; Score 600; DB 10; Pred. No. 4.9e-197; Mismatches Indels plant 0; Gaps 120

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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

ITILE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322.478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
INOMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 12286
TYPE: DNA
TYPE: DNA
TYPE: DNA
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US-09-965-553-17
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Best Local S
Matches 600
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                                                                                     GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                                                                                                                                       TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
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APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087125
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
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Best Local Similarity
Matches 582; Conserv
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97.0%;
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; SEQ ID NO 34
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Glycine m
US-09-965-553-34
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APPLICANT: Voytas, Daniel F.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Plant Retroelements and Methods Rel

FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: US/09/965,553

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-29

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SECTIMARE: Patentin Ver. 2.0
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US-09-965-553-34
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                                                                                            GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                     CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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Pred. No. 4.9e-186;
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; ORGANISM: Glycine
US-09-965-553-19
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US-09-965-553-19
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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Plant Retroelements and Methods Related The

FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: US/09/965,553

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR APPLICATION NUMBER: 60/087125

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19

LENGTH: 9829
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                                                            GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
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94.0%;
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Pred. No. 6.8e-173;
""amatches 35;
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Sequence 20, Application US/0996553

Patent No. US20020112259A1

GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
CITRLE OF INVENTION: Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553

CURRENT ETLING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR APPLICATION NUMBER: 60/087125

PRIOR APPLICATION NUMBER: 60/087125

PRIOR APPLICATION NUMBER: 09/32-478

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

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; ORGANISM: Glycine
US-09-965-553-20
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US-09-965-553-20
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                                                GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCCTCATTTGAC
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                 AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                                     CAAGAGAAGGCGGCCTTTACATGCCCTTTTGGCGTTTTTGCTTATAGAAGGATGCCATTC
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; SEQ ID NO 22
; LENGTH: 9139
; TYPE: DNA
; ORGANISM: Glycine max
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APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF PLANT Retroelement
CURRENT ELING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
NUMBER OF SEQ ID NOS: 41
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Patent No. US20020112259A1
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Similarity 73.5%;
                                                                                     AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAAGGTGCGAAGAGACACTAACTTGGTACTG
                                                                                                                                                      GIGGAGAAAAGCATCGAGGIATITAIGGACGACIICCTCGGITTITIGGACCCCCCATIIGAC
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 AATTIGGGAGAAATTICCATTITCATGGTTCAAGAAGGAATAGTGCTGGGGGCATAAAATTTCA
                                                                    GGGTGCCTATTAAATCTTGAAAGAGTATTACAGAGATGTGAAGAGTCCAATCTAGTTCTC
                                                                                                                                    GTGGAAAAATGCATCGAAGTTTTCATGGATGATTTCTCTATTTTTGGGCCCATCCTTTAAG
                                                                                                                                                                                                       GGTCTGTGCAATGCCCCAGCTACATTTCAGAGGTGTATTATGGCAATTTTTTCTGATATG
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RESULT 9
US-09-965-553-27
Sequence 27, Ap
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TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR PRIOR APPLICATION NUMBER: 60/087125
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Pisum
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                                                                                                                                         TTATGCTTGGCAAACTTGAAAACGGTGCTTGAAAGATGTGTGAAGACCAATCTTGTGCTT
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Application

us/09965553

RESULT 10 US-09-965-553-23

Sequence 23, Application US/09965553
Patent No. US20020112259A1
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.

Methods Related Thereto

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PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020112259A1
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Vytas, Daniel F.
APPLICAT: Vytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
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                                                                ACTACTGTTTCTTGGATGGATACTCGGGGATACAACCAGATCGCGGTAGACCCCAGAGATC
ATTGGGAAAAGTGTCATTCATGGTGAAGGAAGGCATAGTATTGGACCACAAGATATCA
                               ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                                                      TCGAGGAGATGGTGGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCTCTTTCTCCT
                                                                                                                                                                        TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGGTTTTTTGGACCCTCATTTGACA 481
                                                                                                                                                                                                           GTTTATGCAATGCTCCTGCAACATTTCAGAGGTGTATGACCTCTATATTTTCAGACTTAA
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Pred. No. 7.7e-95;
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; ORGANISM: Glycine max
US-09-965-553-23
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                                                                                                                                                                                                                                                                                                                  Sequence 634, Application US/10083357
Publication No. US20030054370A1
GENERAL INFORMATION:
APPLICANT: QLANDONG Zeng et al.
TITLE OF INVENTION: Systemic Discovery of
FILE REFERENCE: 032796-090
CURRENT APPLICATION UNBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 634
LENGTH: 3813
TYPE: DNA
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Best Local Similarity
Matches 215; Conserv
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SEQ ID NO 23
LENGTH: 10482
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CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
     1228
                                                            1168
                                                                                                                     1108
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 TTGCATAGTGGTTACCACCAGATCCCGATGGAACCCCAAAGACCGCTACAAAACCGCCTTT
                                                                                 CGACTCTGCGTCGATTACCGCACCCTGAACAAGCTACCATCTCCGACCCCATTCCCCATTA
                                                                                                                              CGAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCTTA 198
                         GGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGATCAGGAGAAGACGGCCTTT 318
                                                      CCCAGAATCGACAACCTATTGAGCCGTATTGGAAATGCCCCAGATATTTACCACGCTAGAT
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Pred. No. 1.8e
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Pred. No. 5.3e-17;
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US-10-255-536-16
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; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Drosophila
US-10-255-536-16
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Best Local Similarity 46.6%;
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TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related TITLE OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: p-NI 3864

CURRENT APPLICATION NUMBER: US/10/255,536

CURRENT FILING DATE: 2002-09-25

CURRENT FILING DATE: 2002-09-25
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
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                                     GAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGACAGC 483
CCATCGCAAGCATTTCTATATATGGATGACTTAGTAGTAATAGGTTGTTCAGAAAAAACAT
                                                                                                                    CTGAAAGTAGCACCAAACTCCTTCCAACGTATGATGACACTTGCATTTTCTGGTCTTGAA
                                                                                                                                                                                                                                                                                                  GAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGG 363
                                                                                                                                                                                                                                                                                                                                                                 TTTTCATGTCTCGACCTAATGTCTGGATTCCACCAGATAGAACTAGAAAAAAGGTATAGA 284
                                                                                                                                                                             TTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGGTG 423
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Pred. No. 4.1e-13;
0; Mismatches 251
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PRABLISM: Phaseolus coccineus
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(4298)
OTHER INFORMATION: Scarlet Runner Be
NAME/KEY: modified base
LOCATION: (1)..(4298)
OTHER INFORMATION: n = g, a, c or t
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Best Local Similarity 46.3%;
Matches 211; Conservative
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PRIOR APPLICATION NUMBER: US 60/253,672
PRIOR APPLICATION NUMBER: US 60/253,672
PRIOR FILING DATE: 2000-11-28
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APPLICANT: Apuya, Nestor
APPLICANT: Tatarinova, Ta
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TAGTAAAACCCTAGAAGACCATCTAAGTCACCTTAGGGAAGTTCTTCTAGTTCTTAGGAA
                                     TGGACCCTCATTTGACAGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGA 524
                                                                                                        CATTITITCAGACATGGTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTT 464
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Tatarinova, Tatiana
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The Regents of the University of California
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Pred. No.
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Publication No.
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SEQ ID NO 2
LENGTH: 4921
TYPE: DNA
ORGANISM: Phaseolus coccineus
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TITLE OF INVENTION: Polynucleotides Useful
FILE REFERENCE: 023070-115810US
CURRENT APPLICATION NUMBER: US/09/997,672
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/253,672
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 42
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LOCATION: (4347
NAME/KEY: exon
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NAME/KEY: modified_base
LOCATION: (1)..(4921)
OTHER INFORMATION: n = g,
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Similarity 46.3%;
11; Conservative
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TAGTAAAACCCTAGAAGACCATCTAAGTCACCTTAGGGAAGTTCTTCTAGTTCTTAGGAA
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No. US20030061632A1
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Tatarinova, Tatiana
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Pred. No.
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Sequence 1, Application US/09864680
Patent No, US20020012981A1
GENERAL INFORMATION:
APPLICANT: Staskawicz, et al.
TITLE OF INVENTION: B82 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/864,680
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/360,186
PRIOR APPLICATION NUMBER: 09/360,186
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 31491
TYPE: DNA
ORGANISM: Capsicum annuum
US-09-864-680-1
Search completed: June 21, 2003, 00:34:41 Job time: 222.698 secs
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US-09-864-680-1/c
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Best Local Similarity 46.8%;
Matches 153; Conservative
                                                                             24007 GTATTTATTGATAATATTCTGATCTAT 23981
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Pred. No. 2.1e-05;
0; Mismatches 174;
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Score Match Length DB ID 317 52.8 582 17 BH421575 315.2 52.5 727 17 BH423185 315.2 52.5 841 17 BH718174 310.4 51.7 759 17 BH555348	BH435343	BH435343	17	834	51.7	310.4	v	C
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2387	BH709535	8494	9455	7953	3439	4394	8842	6137	40554	вн536770	0867	8097	7641	5478	5647	7649	242	27	BH554612	37	5	4488	035	8272	3074	409	5643	075	648	4354	0165	0345	1145	H59797	9706	44	51
н523876 вонтw89т	535	BASAS BOGLISZT	94557 BOHVI20T	79539	H734399 BOMIH7	43949	88426	н661378	05540	1.1	08673	80975	76412		56471	76493	BH452427 BOGTQ24TR	BH505270 BOHSE73TR	BH554612 BOGUN67TF	вн701377 вомнн20тк	BH449694 BOGQZ15TR	BH244881 AUIJA12TR	BH550351 BOHAK33TR	BH682723 BOMEF67TR	BH530743 BOHQG52TR	BH434092 BOGZS83TF	BH656439 BOMBT94TF	BH420759 BOGIJ23TR	BQ996483 QGG12P10.	BH443545 BOGGG29TR			вонхтє		H697068 BOMOT46T	H714463 BOMPQ54T	BH448511 BOGOM52TF

ALIGNMENTS

FEATURES source		AUTHORS TITLE JOURNAL COMMENT	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BH421575/c LOCUS DEFINITION
Location/Qualifiers 1582	9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: FF Class: sheared ends.	Town/C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHEX22TR Contact: Chris Town TIGR	Brassica oleracea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 582)	sequence. BH421575 BH421575.1 GI:17607303 GSS. Brassica oleracea.	BH421575 582 bp DNA linear GSS 12-DEC-2001 BOHEX22TF BOHE Brassica oleracea genomic clone BOHEX22, DNA

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RESULT 2
BH423185/c
LOCUS
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ORGANISM
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                  AUTHORS
TITLE
JOURNAL
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Best Local Similarity
Matches 416; Conserv
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Brassica oleracea.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 727)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOHHA57TF
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вонна57тг вонн
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/strain="Tol000DH3"
/db_xref="taxon:3712"
/clone="BOHEX22"
/clone=!ib="BOHEX"
/clone=!ib="BOHE"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
120 c 118 g 166 t
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71.6%;
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Pred. No. 1e-87;
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oleracea
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genomic
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sequence.
BH718174
BH718174.1
                                BH718174
BOMGI87TF
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Tel: 301-838-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ.
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Class: sheared ends
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DNA is from a doubled haploid
Seg primer: TR
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                                                                                                                AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                                                                                                                GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGGTTTTTTGGACCCTCATTTTGAC
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301-838-0208
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/strain-"701000H3"
/db_xref="taxon.3712"
/clone-"BOHHA57"
/clone-lib-"BOHH"
/note-"Vector: pHOS1; Site_1: Bst)
genomic DNA inserted into pHOS1 us
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  GI:18816340
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using BstXI
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TITLE
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Brassica oleracea.
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Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
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                                                                                                                                                                                        CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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                                                                                    GTGGAGAAAAGCATCGAGGTATTTATGGACCGACTTCTCGGTTTTTTGGACCCTCATTTGAC
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                       GCTTGTTTGTCAAATTTGTGCAGGGTCCTAGAGAGATGTGAAGACACCAACCTTGTGCTG
                                     AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGGTGCGAAGAGACACTAACTTGGTACTG
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AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCCACAAGATCTCA
                                                                                                                         GGTCTATGTAATGCTCCAGCCACCTTTCAAAGGTGCATGATGTCGATCTTTTCTGATCTG
                                                                         ATTGAGGATGTTGTGGAGGTGTTCATGGATGTTCTCCGTCTATGGATCTTCGTTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica ole
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMG187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Bo_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
1 189 c 150 g 243 t
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Pred. No. 4.4
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1 (bases 1 to 759)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shottpun sequencing of Brassica oleracea
Unpublished (2001)
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Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en Rosidae; eurosids II; Brassicales; Brassicaceae; Bras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea
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GGATTGTGCAATGCTCCTGCCACTTTCCAGAGATGCATGATGTCGATCTATACTGATCTT
                    GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                                                   CAAGAGAAGACAACATTCACCTGCCCATACGGTACTTTTTGCCTACAGGAGAATGCCTTTC
                                                                                                          CAGGAGAAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
                                                                                                                                                                       TACTACTGTTTTCTCGATGGCTACTCCGGGTTCTTTCAGATACCCATTCATCCAGACGAC
                                                                                                                                                                                                               TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT 300
                                                                                                                                                                                                                                                          AAGGACCACTTCCCACTTCATTGACCAGATGCTGGAAAGACTAGCCAACCACCCC
                                                                                                                                                                                                                                                                                                 AGAACAGTCACAGGGCATAGGATGTGCATTGACTACAGGAAGCTAAACTCAGCCACAAGG
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/clone_lib="BO_2_3_KB"
/clone_lib="BO_2_3_KB"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1 using BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
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/strain="TO1000DH3"
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Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSS: BOHAU19TR Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
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                                                                                                                                                                                                                 Similarity 69.8
19; Conservative
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                                                                   AAGGACCACTTCCCACTTCCTTTCATTGACCAGATGCTGGAAAGACTAGCCAACCACCCC
                AGAACAATCACAGGGCATAGGATGTGCATTGACTACAGGAAGCTAAACTCAGCCACAAGG
                                                                                                     GTTCCTAAGAAGGGTGGCATCACTGTCATCACAATGAGAAGGATGAGCTGATTCCTACC
                                                                                                                       GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGGAATGACTTGATACCAACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medical Center Drive, 301-838-3523
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/clone_11b="BOHA"
/note="Vector: pHOS1; &
genomic DNA inserted ir
genomic DNA inserted ir
179 g
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/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHAU19"
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Pred. No. 1.4e-85;
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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BOHBD63TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHBD63TF
                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris Town
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GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                              TTAGATGCAGGAGTAATATATCCTATTTCAGATAGCAAATGGGTGTCTCCTGTGCATGTT
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                                                                                           Conservative
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                                                                                                                                                            /organism="Brassica oleracea"
/strain="701000pH3"
/db_xref="taxon:3712"
/clone="BOHBD63"
/clone=11b="BOHB"
/clone=11b="BOHB"
/note="Vector: pHOS1; Site_1: Feenomic DNA inserted into pHOS1; a 126 c 162 g 230 t
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                                                                                                                                                                                          Contact: Chris Town
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                                                                                                                                              2 Medical Center I
: 301-838-3523
: 301-838-0208
                                                                                                                           il: cdtown@tigr.org
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e genome shotgun sequencing of B
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/clone="BOGOM52"
/clone_lib="BOGO"
/note="Vector: pHOS1; S
genomic DNA inserted in
a 201 c 170 g
                                                  /organism="Brassica o
/strain="TO1000DH3"
/db_xref="taxon:3712"
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           Email: cdtown@tigr.org
                                                                        Contact:
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Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOMPQ54TF
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                                                                                                                                                            Utterback, T.
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                                                                                                                                          I. and Fraser, C.M.
Brassica oleracea
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           Brassica oleracea.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 814)
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BOMOT46TR
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GSS.
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/clone="BOMPQ54"
/clone="BOMPQ54"
/clone="BO_2_3_KB"
/note="vector: pHOS1; Site_1: BstXI; 2
genomic DNA inserted into pHOS1 using
a 151 c 184 g 219 t
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/strain="TO1000DH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOMOT46TF
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             AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                               AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                                  GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGGTTTTTTGGACCCTCATTTGAC
                                                                                                                                                                    GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTTCAGACATG
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                                                 GACTGCCTTGCTAATCTGTGCAAGGTGCTGGAAAGATGTGAGGAAGAACTTGGTGCTA
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/Clone-lib="BO_2_3_KB"
/Clone-lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
178 c 195 g 217 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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RESULT 10 BH597975

LOCUS DEFINITION

BH597975 BOHGL95TR

BOHG

Brassica

805 bp oleracea

genomic

linear clone BOH

ear GSS BOHGL95,

15-DEC-2001

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
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                                                                                                                                                                                       GATTGTGCAATGCTCCTGCCACTTTCCAGAGATGCATGATGTCGATCTTTACTGATCTTA
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/db_xref="taxon:3712"
/clone="BOHG;95"
/clone_1:b="BOHG"
/clon
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/strain="TO1000DH3"
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Pred. No. 8.7e-84;
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Tel: 301-838-3523
Fax: 301-838-0208
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BOHXT83TF BO_2_3_KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
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             AAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 207 c 178 g 243 t
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/db_xref="taxon:3712"
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                          366
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Best Local (
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotun sequencing of Brassica oleraces Unpublished (2001) Other_GSSs: BOMGU48TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
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BOMGU48TR BO_2_3_KB
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea.
                                                                                                                   TACCCTATCTCAGATTCTAAATGGGTATCACCTGTGCATGTTGTACCAAGAAAGGAAAGGTGGT
                          CGAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCCTTA 198
                                                                          ATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACACGAACTGTCACTGGTTGG
AGAATGTGCATTGATTACCGAAAACTAAACTCCGCATCTAGAAAGGATCATTTCCCATTA
                                                        ATCACTGTGATAAAAATGACAAGGATGAA--TGATACCAACAAGAACCATCACAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAAAGTGTCATTTCATGGTTCGAGAGAGGCCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACATTATGGAGGTTTTTATGGACGATTTCTCAGTCTACAGTTCTTCATTTAGCGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAAGTGTCATTCATGGTGAAAGATGGCATTGTTTTGGGTCACAGGATATCA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      il: cdtown@tigr.org
is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                        primer: TR
                                                                                                                                                                                                                                                            217
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          sheared ends.
                                                                                                                                                                                                                                                     /db_xref="taxon:3712"
/clone="BOMGU48"
/clone=1"BDMGU48"
/clone=1"b-"BOD_3_KB"
/clone=1"Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 163 c 144 g 219 t
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .743
                                                                                                                                                                                                                                                                                                                                             /organism="Brassica oleracea"
/strain="TO1000DH3"
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                                                                                                                                                                                               50.4%;
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Brassica
                                                                                                                                                                                 0,
                                                                                                                                                                             Score 302.4; DB 1
Pred. No. 4.1e-83;
0; Mismatches 166
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genomic clone
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BOMGU48, DNA
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483
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                                                                                     138
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BASE COUNT
ORIGIN
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KEYWORDS
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BH501651
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AUTHORS
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Query Match
Best Local Similarity 69.0
Matches 414; Conservative
                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH501651
BOGOH29TR
                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled |
Seq primer: TR
                                                                                                                                                                                                                                                                                                                             Contact:
                                                                                                                                                                                                                                                                                                                                          Other_GSSs: BOGOH29TF
                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                   Town, C.D., Van Aken, S., Utterback, T. and Fr. Whole genome shotgun sequencing of Brassica
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Brassicaceae; Brassica.
                                                                                                                                                                                                                 Class: sheared ends.
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BH501651
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                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 796)
                                                                       222
                                                                                                                                                                                                                                                                        301-838-0208
                                                                                                                                                                                                                                                                                    Medical Center Drive, 301-838-3523
                                                                    /clone_lib="BOGO"
/note="Vector: pHOS1; Site_1: BstXI; 2
genomic DNA inserted into pHOS1 using
a 169 c 191 g 214 t
                                                                                                                                                                                                                                                                                                                           Chris Town
                                                                                                                             /db_xref="taxon:3712"
/clone="BOGOH29"
                                                                                                                                                         /organism="Brassica
/strain="TO1000DH3"
                                                                                                                                                                                                 Location/Qualifiers
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                50.4%;
69.0%;
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 Score 302.4; DB:
Pred. No. 4.2e-83,
D; Mismatches 180
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S1 using BstXI linkers"
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BOGOH29,
                                                                                                                                                                                                                                                                                                 USA.
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TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BH443545/c
                                                                             FEATURES
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TITLE
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                                                               source
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                                                                                                                                                                                                        1 (bases 1 to 800)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGGG29TF
Contact: Chris Town
                                                                                      Seq primer: TR
Class: sheared ends.
                                                                                                                     Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sociale; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                           Brassica oleracea.
Brassica oleracea
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BOGGG29TR BOGG
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: 301-838-3523
: 301-838-0208
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    /organism="Brassica oleracea"
/strain="TO1000H3"
/db_xref="taxon:3712"
/clone="BOGGG29"
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                                                                         Location/Qualifiers
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                                                                                         AUTHORS
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QGG12P10. mRNA sequence.
QGG12P10, mRNA sequence.
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BQ996483.1 GI:22430879
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elli:
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
                                                                                                                     Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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/note="Vector: pHOS1;
genomic DNA inserted:
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egle,J., Ellison
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Best Local Similarity .69.6%;
Matches 409; Conservative
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552 GTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTC 599
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                                         481 AAACCTGACTGCGGTATTGCAAAAGTGTGTTCAACATAATCTTGTGCTAAATTGGGAAAA
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singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QGG12 row: P column: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asmundson Hall, UCD, 1
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA '95616, USA
                                                                                GAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGAATTGGGAAAA 551
                                                                                                                       TGTTGAAGTCTTTATGGATGATTTTTCAGTCCATGGTGATACATTTGAGAGTTGCTTGAA 480
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                                                                                                                                                               CATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACAGCTGTTTGAG 491
                                                                                                                                                                                                        TGCCCCAGCTACATTCCAAAGGTGCATGATGTCTATTTTTTCAGACATGGTTGAAAATTT 420
                                                                                                                                                                                                                                TGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGGTGGAGAAAAG 431
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/lab_host="E.col1"
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/clone="QGG12P10"
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/cultivar="L.serriola"
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Search completed: June 20, 2003, 22:39:20 Job time: 2307.77 secs

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REFERENCE AUTHORS 1 (bases 1 to 10128) Wright, D.A. and Voytas, D.F.

Pred. No. is the number of results predicted by chance to have a

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Wright,D.A. and Voytas,D.F.
Direct Submission
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Address for correspondence: koos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MVAll
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
RetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.lastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE).
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Arabidopsis thaliana genomic
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AP001311.1 GI:7209747
                                                                                                                                                                                                                                                                                                                               shorter because we remove overlaps between neighboring submissions. The 5^{\prime} clone is T6J22 and the 3^{\prime} clone is MSJ3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-MAR-2000) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                      This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 83339) Kaneko, T., Kato, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
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                                                       /clone_lib="Mitsui p1" complement(join(1709.
2612. .2790))
/note="gene_id:MVA11.1
                                                                                                                    /clone="MVAll"
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/chromosome="3"
                                                                                                                                                                                                          organism="Arabidopsis/strain="Columbia"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Pred. No. 3.2e+02;
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by 90 P1, TAC
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	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	
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18	Query Match 100.0%; Score 18; DB 8; Length 83339; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	LIGGDFRQILPVIPQRTRQETVSAAINRSYLWESCHKYLLSQNMRVQPEEIKFÄEWIL QIGDGEAPRKTHGIDDGEEDNIIIDKNILLPETENPLEVICQSYSPDFTNTFQDLEN LKGTAVLTPRNETVDEINDYLLSKYPGLAKESYFSADS IDQDEALTEEGFFENSYPMEYL NSLEFPGLPAHRLCLKVGVPIMLLENLNQKEGLCNGTRLTVTHLGGKVLKABILSDTT KKRKKVLIPRIILSPODSKHPFTLRROCPVRMCYAMTVNKSQGGTLNRVALYLPKPV ESHGQLYVALSRVTSPKGLTVLDTSKKKEGKYVTNIVYREVFNGLPAITGKKS" BASE COUNT 26491 a 15765 c 14391 g 26692 t ORIGIN	/evidence=nol_experimendal /protein_id="BaB02227.1" /protein_id="BaB02227.1" /db_xref="GI:9294330" /db_xref="GI:9294330" /translation="MEVLDSTMMYTRKORENIGRIVNILPTAGDLYYLRILLNKVK /translation="MEVLDSTMMYTRKORENIGRIVNILPTAGDLYYLRILLNKVK GANSEDYLKTVGGVVHESSKAACHARGLLDGDKEWHDAMDEAAOWSTSYLLRSLEYVLI GANSEDYLKTVGGVVHESSKAACHARGQRVLNFPQLELKAKELBKYTLIEIETLLRQ LIYCEVSEPLKLMSHCWESMADDVLRKQQRVLNFPQLELKAKELBKYTLIEIETLLRQ HEKSLSDYPEMPQPEKSNGKNVMPVASSALAALLLPGGRYAHSWFKIPINVHEDFICD IKIGSMLANVLSKVDLIWDEAPWAHRHFPEAVDRTLRDJLSVGDEKALTKTLGGKTVV	CDS join(773457871.7810679438) /note="contains similarity to unknown protein gb Aa5621.1 gene_id:MVA11.17" /codon_start=1	/protein_id="BAB02226.1" //db_xref="G1:9294329" //tanslation:"MCIGPRESQKTYEPKGPKKTQLKLQTLDFIF8NSIDAIQRTTKE /translation:"MCIGPRESQKTYEPKGPKKTQLKLQTLDFIF8NSIDAIQRTTKE KKSYSYTAFWSFPYFSSPEAQTSTVVGRLLRFWDANNIKKDGQFMGIVLLLLDEKCSE KKSYSYTAFWSFPYFSSPEAQTSTVGRCTKLYKITDHPFLLRFLFATTIIEVS IHAFIPAALASHFRQVLREGIIFNVSGFEVGRCTKLYKITDHPFLLRFLFATTIIEVS DVGPTIEREKFMLRNFDNLQALASHTTLELDVVGQTTFVQNSUNLNDTSTQKLVLRYK TDSSVITVYLSLLDDVAATFRAHLSSGDTTLYSVMLTTVANDKMFGG"	/note-"abj AnA25622.1 /note-"abj AnA25622.1 gene_id:MVA11.16 strong similarity to unknown protein" /codon_start=1 /cvidence=not_experimental		/pseudo /codon_start=1 /evidence=not_experimental /product="retroelement pol polyprotein" complement(join(701417033,7073770900,7105471187, complement(join(7014170366,7219972289,7234472573))	/evidence=not_experimental /evidence=not_experimental /protein_id="BAB02225.1" /db_xref="GI:9294328" /translation="MGFKTLPSLIPQKLMDHGLPFDTPAAAVERGTTPLLNYVFAELKD /translation="MGFKTLPSLIPQKLMDHGLPFDTPAAAVERGTTPLLNYVFAELKD /ATEIQSAGLVSPTPIIIGKVVELSPLWPHCMKESSCLVETQ" complement(6324666054) /note="gene_id:MVA11.14"	gene_id:MVA11.12" /pseudo /pseudo /codon_start=1 /evidence=not_experimental join(5931159421.5952259671) /note="contains similarity to uroporphyrinogen III methyltransferase gene_id:MVA11.13" /codon_start=1	CDS complement(join(5756857707,5777957928,5805158165, 5827658305)) /note="contains similarity to disease resistance RPP5 like

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REFERENCE
AUTHORS
TITLE
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AC006413
AC006413.4
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Submitted (27-FEB-2002) The Institute for Genomic Research, Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or. Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or. On Apr 18, 2002 this sequence version replaced gi:6598560.

Location/Qualifiers
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Direct Submission
Submitted (09-MAR-2000) The Institute for Submitted (09-MAR-2000) The Institute for No. Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 106716)
1 (bases 1 to 106716)
1 Lin, X., Kaul, S., Shea, T.P., Fujil, C.Y., Shen, M., Vanaken, S.E., Barnstead, M.E., Mason, T.M., Bowman, C.L., Ronning, C.M., Bentto, M.-I., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D., Nlerman, W.C., Fraser, C.M. and Venter, J.C.
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Town,C.D. and Kaul,S.
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Arabidopsis thaliana chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="ve013"
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.>1187
                                                                                                           al protein"
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/rpt_family="(GA)n"
/rpt_family="(GA)n"
/rpt_family="(GA)n"
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L12220)"
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join(<5036. 5176,5353. 5464,5508. 5702,5873. 5973,
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                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(14369. .14687,14776.
/gene="At2g06200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQKEKEESNGEAGDPNMEEEEEEEEAN" complement(12724. .12818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIHLTPSNYTFRFDLGAVMQKSSSSTLQKKKRTADEVRSTVAEAENAVRVFTQLSAAS
DLHVHGFDSKKIQTHVQYCSHLLEAAKVHREAAEQEELQNRQRLEVARQAALAEEARR
KAEEQRKYQLEKRKQEEELRRLKQEEEKFQRIKEQWKSSTPGSNKRKDRVEDDDGESK
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EYHEKYLLDSLLEDDYDDDLDLIDIYIDNWKGRLFYEKKKIWWKGMFPELDAVVASIN
SLTQMMTKGFEETRDKIDAIDGRYKSIELFVADLKEKKHGKQTEEESQHGKQTEEEVF
                                                                                                                                                       QGSKRFYRFLDEWPSSKSSVSTSLFI"
                                                                                                                                                                                                                                                                                                  /product="expressed protein"
/protein_id="AAD19769.2"
/db_xref="GI:20197770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAEEPVDDDAHDLLAAAGLEDPDVDDDEVPTSGVRRRRALSSSDEEGELMEESHPNSS
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/protein_id="AAM15237.1"
/db_xref="Gi:20197768"
/translation-"MASYXIPYQNSEEEVRYVLDQLPRDASDILDILKAEQAPLDLWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YASPEGCYTIKRQQPLDIVVYREPSPEVAKNSKYNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/note="Putative Ty3-type retrotransposon,

structure:

Long

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AP004483/c
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      DEFINITION
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                                                                                                                              49148
AP004483 122116 bp DNA linear PLN 14-DEC-2001 Lotus japonicus genomic DNA, chromosome 1, clone:LjT13004, TM0016,
                                                                                                                                                1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                 Similarity
                                                                                                                              TGGCGCCGTTGTCGGGGA 49131
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                       complement(join(23597. .23821,24081.
25986. .26243,26258. .26464)).
/gene="Att2g06170"
                                                                                                                                                                                                                                                                                                                                                 complement(join(<23597.
25986. .26243,26258. .>;
/gene="At2906170"
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(23597. .26464)
/gene="At2g06170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRRSSGRSQGRGRGSRGRGPNRSQEVRQTSNLGGGSAGNRPFHWSYTHDRDHPIIEDK
AGLANLLRHIKGRNCQVPGDCCYKQVGCSLRATSKQGSFGERARRREDPHLGVDSERE
VRSGARGIVPGMLRLKMELSTSKDLEKGYAEKIKIMEQEFRGLEADKOMARNQHRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKPKKKAPKOKĞSLPMINNDLEVLDSGGGDYDTPKVAAVTQERAGGVGLCLROFLRE
MMAVLPDSGYHBERDALLPRLAFLSSNYSKFRPPRAGYYY PGLRCEQRI KLPRPAAALSG
QDQRQERPRDVLHKCSSWI SDPRWSEGLSGYKLASQI LLLQGGHSVGDFDPARI TRT
QDQRQERPRDVLHKCSSWI SDPRWSEGLSGYKLASQI LLLQADPVIALPAAQPDPLE
CKNQRNHFFRDETLSYDPSSKLSNKLATFNRDRNYTALPIDPADPVIALPAAQPDPLE
EVPQLYFRPSAYFQKKNEVTKSSCSTSQCGTSARAGDLSAVVAAARTSLAASHTQAST
SHPSLAPANARPLLARRARLLPVVRLTAELIYIDQFVAPSREERFKFLAANPEAAVSV
DBBGSGEGOGDEGGEGORDGOWLGGWUNGGRUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTRLFSAPHLTAQIRRGEEISTISKIYVMMASLNNFPHLHSISR
QLTRLPSDLDDSQNKSNHSYGDDDSSSKMRSAASSRQEPRRVITLGGMGPIRRPSTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative Ty3-gypsy-like retroelement
polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(17533. .17932,17938. .18380))
/gene="At2g06190"
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/gene="At2g06190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMLVVRPMNVDEQGTPIGLDEFGSNKDTFPRGLEEDPGTVFATPAGGSKECHG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKKDELSKRYLDLTSIAQGYNKAVHDAKVELAASYSKLLSGIKDKWYAKKEFTVLESQ
AAEVESNLALIDQIVKAAVDLTVEKPRFQAEIDDVEARCTLKEVSDFTLSKLDIPEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="AAD19757.1"
/db_xref="GI:4388719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFKVLRKINDNAYVVALPKSMNISNTFNVADIHEYHADGVLYPEENLRTSSSEVEETD
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VKEVVKAKLEATGKKNKVAADKRRRFKVFKEGDDVMVLLRKGRFAVGTYNKVKPRKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD19756.1"
/db_xref="GI:4388718"
/translation="MDFVLGLPRTQRGVDSVFVVVDRFSKMTHFIACKKTADASNIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g06180"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<19174. .19325,19483. .19702,19717. .20174,20300. .20483
20634. .20843,20930. .21110,21129. .21302,21427. .21586,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="At2g06180"
/note="F5K7.6"
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                                                                                                                                                                                                        Score 18; DB b;
Pred. No. 2.3e+02;
Pred. No. 2.3e+02;
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.21110,21129. .21302,21427. .21586.
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VERSION
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AP003054
                       COMMENT
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52966 TGGCGCCGTTGTCGGGGA 52949
                       Direct Submission
Submitted (20-DEC-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Mar 16, 2001 this sequence version replaced gi:11967926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148246 bp DNA linear Oryza sativa (japonica cultivar-group) genomic DNA, ADDOCOCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, clone:P0436D06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb
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                                                                                                                                                                                                                                              Published Only in Database (2000)
2 (bases 1 to 148246)
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                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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/clone_lib="LjT library"
/note="TAC clone:TM0016"
, 23562 c 23033 g 38363 t
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/db_xref="taxon:34305"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Magnoliophyta; Liliopsida;
Oryzeae; Oryza.
sequence version replaced gi:11967926. from the integrated results of the following:
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Pred. No. 2
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s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 122116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poales;
                                                                                                                                                                                                                                                                                                                                            chromosome
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTP2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC (clone. This sequence of P0436D06 clone has an overlap with P0507H06 (DDBJ:AP003144) clone at 5' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWFMVYKVGMGNAGAALSVSICDWVEVTVLGLYIVLSPSCEKTRAPLTWEAFSGIGSF
IRLAVPSALMILEWWSYELLVLLSGILPHALETSVLSISGSSYRVSNELGAGNPEGA
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IGQQPEIASEVGKYALWLIPGLFAFTYAQCLSKFLQTQSLIFPMYLSSSITLALFIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19066. .19338,19622.
21788. .22330,25632. .25949))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYHLNLKQKVITIAALAPKRPPSLRKPAVIVPVFDNRSAPVVAKQGKDWKEAVVVQHR RHPSHSTRATRGQDIWYRGSQSQYRIKNHSWAISLDFVETIDKSTKSG" complement(join(19066 ...19338,19622. ...19876,20096 ...20179,
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                                                                                                                                                                                                                                                                                                                           join(30567. .30579,31283. .31494)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to Arabidopsis thaliana Chromosome 1, F9L1.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(19066. .19338
21788. .22330,25632. .25949))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             youn(1618. .1860,2195. .2404)
/gene="P0436D06.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note-"hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="P0436D06"
                                                                                                                                                                                                                                                                                                       'note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MASPCTCRAKLNMVSVDSVTTLPKRRAPTYCPERSSISITDLPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                   .30579,31283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                      .31494)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(46544. .484
/gene="""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38066. .38853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="Bab33269.1"
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KEASSSDSADKEVQPEKTMPQEHCDTRLLSFPQRSRKPSVDEQLARFVEVIQKIHINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQCSMDKVRVESVEYSSGRSGATQDGQPVEVHAEFPREGNNDAQEPLLEDAGKTTHTG
QEARANSEEAALRTKANEGVEGEAKDARS ITSBDGMERRLSRLEKGSGSSSSHHDES
STRSSAVVSWEDAKAPRILMGTD LDHVNDRERGAYYMLSDWEYAHTREVSPELLKRI
GYHLYNYRELTIPLQTIEESRAGGAYRETRNMARNERKSSSSTPVQISSGVPPSPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(38856. .43616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0436D06.6"
complement/???
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complement(36243. .37369)
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                                                                                                                                                                                                                                                                                                                                    join(57860...57947,57977...58160,58266...58488,58712...58743,59094...59199,59234...59612,59620...59747,62210...62476,62757...63233,63954...64091)
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59094. .59199,59234. .59612,59620. .59747,62210. .62476,
62757. .63233,63954. .64091)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pseudogene, retrovirus-related pol polyprotein from retrotransposon 17.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(52237. .53379)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MERGGPCDGLCRFRIHLGTRGDCPLPAGGGVQVGWLGLFNVV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="probably inactive due to stop codon in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(46544. .484
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/note="3/ LTR
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JOURNAL
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AUTHORS
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AUTHORS
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Best Local
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                  Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8802, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, rel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a valiable and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                             Published Only in Database (2001)

2 (bases 1 to 189744)

2 sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (02-MAY-2001) Takuji Sasaki, National Institute of
Submitted (02-MAY-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (clone:P0664F03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP003577

189744 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 6
*** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP003577.1 GI:13936417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lone: P0664F03
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the finished
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VRDQTTBCAVCRGAFDTAELLRVLSQCQHAFHGCIDVWLMTHSACLIVCRRSAADGAL
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PPTFKTMADKTLREFAAPSAENVAIGPQINMGDVDFDLKSSLITMAQASPFCGKPNED
ANAHLQQFPEICCTYTIKGNEYNGLIPMSRDHLDAAAGGAFFSKTYQGAVDLIEKLVS
NMGWSERLQJTQRGKMTYTKFTTAFAKLDLLMKCLDDHDKRPQGTVLALDSHVTCEV
VGKAPSSPWTHMLRVRSTATRVILGMTARKPVRRRCIWATTITGTVHKEVRGGTSHAR
TIKELDDILANTLYPMSWYFEKTPQTAELLTTVRHDHTTGLNTEBYPP"
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complement()oin(6849. .66972,67147. .67435,67625.

68423. .68608,71933. .71987,72830. .72928))

/gene="P0435D06.11"

complement()oin(66849. .66972,67147. .67435,67625.

68423. .68608,71933. .71987,72830. .72928))
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/db_xref="GI:13359050"
/translation="MCVDFTDLNKVCPKDHFPLARIDQLVDSMAGCELLSFLDAYSGY
/translation="MCVDFTDLNKVCPKDHFPLARIDQLVDSMAGCELLSFLDAYSGY
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similar to Oryza sativa Chromosome
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/gene="P0436D06.10"
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complement/65222
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sequence as soon as it is available and
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Pred. No. 2.2e+02;
Pred. No. 2.2e+02;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (15-MAY-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DN clone:OSJNBa0031C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP005160 194640 bp DNA linear HTG 17-MAY-20 Oryza sativa (japonica cultivar-group) chromosome 7 clone OSJNBa0031C24, *** SEQUENCING IN PROGRESS ***, in ordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
 . Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA. clone:OSJNBa0031C24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki, T., Matsumoto, T. and Katayose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (2002)
2 (bases 1 to 194640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrhartoideae; Oryzeae;
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Conservative
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40138 c 40698 g
                                                                                                              /db_xref="taxon:39947"
/chromosome="7"
                                                                                                                                              /organism="Oryza sativa
/cultivar="Nipponbare"
                                                                                                                                                                            1. .194640
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/chromosome="6"
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                                                                                            /clone="OSJNBa0031C24"
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Pred. No. 2.1e+02;
                  Pred. No.
                               Score 18;
 Mismatches
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                2.1e+02;
                                                                                                                                                            (japonica
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   Indels
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AF427791/c
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                                                                                                                                                       gene
                                                                                                              CDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 261265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei,F., Wing,R.A. and Wise,R.P. Genome dynamics and evolution of the Mla resistance locus in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-OCT-2001) Plant Pathology and Interdepartmental Genetics, USDA-ARS/Iowa State University, 351 Bessey Hall, Am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wei,F., Wing,R.A. and Wise,R.P. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare Mla locus, complete sequence. AF427791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Cell 14 (8),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF427791.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Stowaway.1; miniature inverted transposable
element-like sequence; type Stowaway"
/rpt_family="MITE"
                                           /note="predicted by GenScan; similar to barley glycine-rich RNA binding protein, CAA88558, pathogen
                                                                                                                                                                                                   element-like sequence;
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                          /Protein_id="aam74515.1"
/Protein_id="aam74515.1"
/db_xref="GI:21672287"
/translation="matiydiglgagenilmatifilifaflrlqpindriffpkwyl
/translation="matiydiglgagenilmatifilifaflrlqpindriffpkwyl
/translation="matiydiglgagenilmatifilifaflkmpeebliehagldsvyylriy
KGMRDSPSSAgaAVTKYVLNVRSYLKFLSNMPAALKMPEEBLIEHAGLDSVYYLRIY
LTGLKIFVPITILAFAVLVPVNWTNDTLEGLKVVHSDIDKLSISNIPYGSKRFIAHLV
MAYVETFWTCYYLKNEYERVATMRLRFLASEKRRPDQFTVLVRNIPPDDESVSELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2585. .2898))
/gene="711N16.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence-not_experimental complement(join(<476. .581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted by GenScan; similar to Arabidopsis
predicted proteins AAD36947 and BAB02357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_type=dispersed
complement(<476. .2898)
/gene="711N16.16"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/chromosome="5"
                  response protein"
                                                                                       /gene="711N16.15"
)oin(4045. .4080,4158. .4466)
/gene="711N16.15"
                                                                                                                                                                                                                       /note="Stowaway.2; miniature inverted transposable
element-like sequence; type Stowaway"
                                                                                                                                                                                                                                                                                          HEELVNHPDHYLKHQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="BAC 711N16; BAC 80H14"
/clone_lib="HV_MBa-Library, Cl
                                                                                                                                                                         'rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hv711N16.16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IA
                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trna
                                                                                         repeat_region
29590 .29746 note-miniature inverted transposable element-like sequence; Type Hormitel levidence-not_experimental /rpt_family="MITE"
                                                                                                                                                                                                                          /evidence=not_experimental
complement(25299. .25490)
                                                                                                                                                            maturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8748. .8829
                                                                                                              evidence-not_experimental
                                                                                                                                                                                note="predicted"
                                                                                                                                                                                                       /gene≖"Bmta
                                                                                                                                                         edicted by Blastx truncated gene"
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SPRIGARSPGGTLSSRONLAGASNYLGYNGVGSPTGASSLQMPIDPLYLQYLAAQVAA
SYDDPFMASGHLGSSYMDLLGPQKGCLSPLLOSQKNYGCYGNLGFGLGYAGSPLTSPV
LPSSPVASGSPLRHGERSMRFASGMRNEGGSFGSWSPDMVGKMEGNLMPSLLEEFKSN
KSRTYELSEIAGHVVEFSADQYGSFFJQQKLETASTEEKDMVFSBIMPQALTLMTDVF
GNYVVQKFFEHGSTTQIKELSDQLIGRVLALSLQMYGCRVIQKAIEVDLAQQTKMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MATRGGEAVCGGGVGGEEGERGDFELFRSGSAPPTVEGAMAMAAGGGGEVLLDDELRADPAYQSYYYSNAHLNPRLPPPLLSKEDWRSASTASAPPPPPPGSAGSATAAGGRRGTGSSACPGSTTPASAASPPSSSILLSVLSVSAYERTTEVCGGQLNDSKFIAVHTSCVHELPLHTLQEDSNQDVDDQDSANHSRNDFLDSSGMQXALHRDTGAMAGGLQRESNEQTLADIRNNELSSHASASPDPELVRRVPSPCLPPLGVKVGAYDKKSNGGSSFRRSSSAVGEPDDLVAALSGMNLSSSRAGNGQAMDQSKLYQDVDNANRYLFDRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"puf family; predicted by GenScan; similar to
Arabidopsis putative pumilio/Mpt5 family RNA-binding
protein AAC95220 with barley matches ESTes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(15373. .15413,15516. .15690,15778. .15972, 16919. .17029,17133. .17345,17868. .17975,18057. .18198, 18994. .20019,20053. .20234,20869. .21007,21065. .21468))/gene-"Bpm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hv711N16.15"
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/protein_id="AAN22835.1"
/db_xref="G1:20513874"
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                                                                                                                                                                                     LEHCDDPTTQQIMMDEILQSVCLLAQDQYGNYVVQHVLEHGKPHERTAIIDKLIGQIV
QMSQQKFASNVIEKCLAFGNPVERQILIGEMLESTTESEPLEVMMKDQFANYVVQKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(15373. .21468)
/gene="Bpm"
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complement(join(9078. .9315,
/note="predicted by GenScan;
                                                                                                                                                 ETCDDQQREMILTRIKAHLNTLKKYTYGKHIVARVEKLVAAGEKRQGLQPACTAA'
                                                                                                                                                                                                                                                                ELDGHIMRCVRDQNGNHVIQKCIECIPQDIIQFIVSTFYGQVVLLSTHPYGCRVIQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mkianallllyslalvylssssthtpsmyegravvypaadcsyt
VIGRGEKCEPRKCEAECRROHDGMGACAAMGCSCAVCAKEASTHTAKPPLIAKSPHHH
RTPPMRHRTSASHTAKTYSWSPPQYPDSSTTRDCYKLSSASEMSPSVAATRYSKEEPD
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/note="predicted by Blastx
maturase; truncated gene"
                                                                                                              complement(22721. .22903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQTSGNQQHSFMKRPEQGHFRAPEGYSANSANSSMMRNQMNAGNFTSSDNSSVGSGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAM22812.1"
/db_xref="GI:20513851"
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/product="HY711N16.14"
/protein_id="AAM22811.1"
/db_xref="GI:20513850"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evidence=not_experimental
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                                       search; similar to Poaceae
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search;

similar

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Poaceae

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RESULT 10
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     DEFINITION
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                                                                                                                                                256409
                                                                                                                                                                                                                                                                          Local
AP002458 67517 bp Arabidopsis thaliana genomic DNA,
                                                                                                                                                                                                                                                 l Similarity
18; Conserv
                                                                                                                                                   TGGCGCCGTTGTCGGGGA 256392
                                                                                                                                                                                                   TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=dispersed 49126. .49163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            element-like sequence; type Stowaway"
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="partial; part of polyprotein and 3' untranscribed
or translated region deleted, the LTRs are intact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="coding region not determined; predicted by BLASTn
and EST search; barley DCINA-induced gene; similar to th
sequence deposited in GenBank Accession Number AJ250665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=dispersed <29965. .>30140
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Hormites3.1; miniature inverted element-like sequence; type Hormite3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37785. .39765
/gene="711N16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRRYGROASLGPPDTTDLSGYDAAVGCRVRMDGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPRRPPTLSCSVAIRTARVVPLGRSCWEDFGSQAEVMGGHDEVK
LVQFKPAAIDCSVQRPFPAIVVHLQMLHGVARVYRRRRSRGGDIGARLYDGVVVVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/rpt_family="HORPIA-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence; type Hormite2"
                                                                                                                                                                                                                                                                                                                                                 /note="Hormites3.2; miniature inverted transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Stowaway.3; miniature inverted transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jóin(37785. .37972,38394. .38577,39727. .39765)
′gene="711N16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transposon="Ac-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="miniature inverted transposable element-like
                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposon="Copia/Gypsy-like retrotransposon BARE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="BARE-1 SoloLTR-1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="5-bp insertion signature (BARE-1 SoloLTR-1.2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAM22813.1"
/db_xref="GI:20513852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="HV711N16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="predicted by GenScan; function unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transposon="Copia/Tyl-like retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_type=direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note-"incomplete ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'evidence=experimental
                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insertion signature (BARE-1 SoloLTR-1.2)*
                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                          2e+02;
  chromosome 3, BAC clone:T22C2.
                                                                                                                                                                                                                                                                                                 DB 8;
                           DNA
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, pl
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=T22C2
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=T22C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUN-2000) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP002458 BA000014
AP002458.1 GI:83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes with similarity to proteins in the databases are described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:TAMU BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural Analysis of Arabidopsis thaliana Chromosome 3. III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 67517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T because we remove overlaps between neighboring submissions. clone is T22B15 and the 3' clone is T1013.
                      /evidence=not_experimental

complement(1423. 1696)

/product="(+)-delta-cadinene synthase (d-cadinene

synthase) like"
                                                                                                                                                                                                 /evidence=not_experimental

complement(909. .1318)

/product="(+)-delta-cadinene synthase (d-cadinene

synthase) like"
                                                                                                                                                                                                                                                                                                                     /note="CDS is reported in
gene_id:T22B15.28"
                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
complement(423. .758)
/product="(+)-delta-cadinene synthase (d-cadinene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="CDS is reported gene_id:T22B15.28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(32.
/product="(+)-c
                                                                                                                                              /note="CDS is reported in gene_id:T22B15.28"
                                                                                                                                                                                                                                                                                                                                                                   synthase) like"
  /note="CDS is reported in Acc# AP002062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthase) like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="TAMU BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:8347610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (+)-delta-cadinene synthase (d-cadinene
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CDS
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/product="(+) celta-cadinene synthase (d-cadinene
synthase) like"
/note="CDS is reported in Acc# AP002062
gene_id:T22B15.28"
                                                                                                                                                                                   complement(join(34053. .35108,35292. .35906))
/note="contains similarity to non-LTR retroelement reverse
                                                                                                                                                                                                                            /translation="MGADIVADGLTDRPPDRLADEPAEGLSDRLPEGLSEEPADELVD
KLNLTKEPHDVLEDFLLFIFTLMKTTRHLGAAEMTHILFTHPKPREKNLSLIGGSLAF
SLKIEYSPLDPVCLLTLEDLSKT"
                                                                                                                                                                                                                                                                                                                                                                        gene_id:T22C2.7
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
complement(30211..31032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"contains similarity to unknown protein emb|CAB77997.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONGGEEQADDDDDEEHPQTYHN"

complement(join(15703. .16226,16332.

17792. .17980,18269. .18867,18953. ..

20974. .21359))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPRRQNLRSIVASMPRIWGQSGLVHGRIMEGRQEHFIFTLEESLETVLRRGPWAFNDW
MILLQRWEPQIPLFPFIPFWVQIRGIPFQPLNRGVVEHIGRALGQVLDTDENVEVVAR
MDFARVLLHWDITHPLRFQRHFQFTAGVNTLLRFRYERLRGFCEVCGMLTHDFGACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(11186. .11911)
/note="gene_id:T22C2.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental complement(join(3258. .7313,8240. .8346,8681. /note="gene_id:T22C2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene_1d:T22B15.28"
                                                                                                                                            gene_id:T22C2.8"
                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
33467. .33844
/note="emb|CABB1790.1
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/protein_id-"BAA97081.1"
/db_xref-"Gi:8777563"
/translation-"MADNLRRAVQDINLGVDDIPFALPEDIVNHAVAENRFILFGRPV
                                      /codon_start=1
/evidence=not_experimental
/oin(35982. .36259,36422.
/note="gene_id:T22C2.9
                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/protein_id="BAA97082.1"
/db_xref="GI:8777564"
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/product-"helicase-like protein"
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                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                   ||T01474
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unknown
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                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                     RESULT 11
AF028277
                                                                                                                        DEFINITION ACCESSION
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                                           ORGANISM
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Best Local
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17; Conserv
                                                                                                     AF028277.1
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43810 TGGCGCCGTTGTCGGGG 43826
Hordeum chilense.
Hordeum chilense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                     Hordeum chilense RAPD marker AF028277
                                                                                                                                                                                                                                                                                                                                                        TGCCCCCGTTGTCGGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSSDNFFTFASFEDIKSGSLDTNICVGTKTYRNVLVYKYYRRNQ NDEGPPDNEWWBIFFDIENVECDKLTCKLLKAYANDFFDNWRHCVDKIIICVMRFAKL KVDQGLASQDGARLYESFIEPSMCRS"
join(48668. 48804,48893. 49148,49230. 49299,49414. 495649794. 49928,50041. 50200,50258. 50423,50538. 50697,50757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MALDTASNGEFMTKTETEATKLIENLAGSNSNHNVDYDRSNRGG
GGESKGPAELAKVEQLMRRDORSVNFCEDSSKGMVHGEFSGDGSEDLQAEIRVNGS
TNVENPODDYVFPTQAGSGGOKEQPVEFQNKGKYVGGPCPPAGTGHASSETDNEMKLMA
QVLEDQKKNAADINVKVDSMYNDLNGKFATLSSHVKTLENQVSQIVSASMRPDGTHS
GKYKFRGKEQCYAIMIQEELAEIVVAKQVETNVVVETLVEDKIVEDDEPLSVEPPPY
VPKLFFPGRERQIQRKEYARFDEIMKQLYVRLFFIQDLHVPSYRSYKKYLIENKRS
IEEGVKLISKGEHAQLVESQNKQQKEAQTNVVFTLYDFSYRSYKYKILSNKRS
IEEGVKLISKGEHAQLVESQNKQXEAQTNVARVGNETIPTHYESXRSYKYLIENKRS
IEEGVKLISKGEHAQLVESQNKQXEAQTNVARVGNETIPTHYELENXEPHDDLNLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene_id:T22C2.13
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AHVILIPLQRVEDTIEYKVQCKGTSKPFSKARSILTSEMKEKGRKAVKRVVGKVLKMK
LTDWRPCEGASSRTRVH"
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complement(join(40707. .41698,41792.
/note="gene_1d:T22C2.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
join(51608. .51745,51834. .52098,52211. .52313,52391.
/note="gene_id:T22C2.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to unknown
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/protein_id="BAA97084.1"
/db_xref="GI:8777566"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(47271. .47464,47537.
/note="gene_id:T22C2.12
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/protein_id="BAA97083.1"
/db_xref="GI:8777565"
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/product="retroelement pol
join(44238. .44539,44606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="replication
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/codon_start=1
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                                                                                                                             GI:4581593
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.50200,50258. .50423,50538. .50697,
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7.2e+02;
0;
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.45477,45594. .45890,45945.
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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KEYWORDS
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SOURCE
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AUTHORS
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ACCESSION
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Matches 17
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                     22
       Brassica nigra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1732)
Bhanot, R., Srivastavs, P.S., Delseny, M., This, P., Singh Negi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       687 bp
Sequence 13 from Patent WO0055325.
AX059280
                                                                                                                                                                           X89901.1 GI:927389
Transfer-RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity 94.4
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preuss,D., Copenhaver,G. and Keith,K. Plant chromosome compositions and methods Patent: WO 0055325-A 13 21-SEP-2000; The University of Chicago (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pooideae; Triticeae; Hordeum.
1 (bases 1 to 537)
Hernandez,P., Martin,A. and Dorado,G.
                                                                                                                                                                                                                     B.nigra DNA for tRNA like
X89901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Spermatophyta;
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-OCT-1997) Agronomia y Mejora Vegetal, Instituto de
Agricultura Sostenible (IAS), Avda. Menendez Pidal (Alameda del
Obispo), Cordoba 14080, Spain
                                                                                                                                                    black mustard.
                                                                                                                                                                                                                                                                BNDNATRNA
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Lakshmikumaran,M
                                                                                                                                                                                                                                                                                                                                                                                                          TGGCGCCGTTGTCGGGGA 18
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                                                                                                                                                                                                                                                                                                                                                                                   TGGCGCCGTTGCCGGGGA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
135 c 115 g 196 t
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/strain="H1"
/db_xref="taxon:15565"
/clone="IAS-pHCR9"
83 c 111 g 193 t
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1. .687
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ke gene.
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No. 2.
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                Singh Negi, M.
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                                                                                                       Tracheophyta;
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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Direct (24-JUL-1995) M.S. Submitted (24-JUL-1995) M.S.
                                                                                                                                                                                                                                                          Ivashuta, S. and Naumkina, M.
Direct Submission
Submitted (23-OCT-2001) Graduate Schouniversity, North-9 West-9, Kita-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago sativa LTR retroelement MCIRE hypothetical complete cds. AF439379
                                                                                                                                                                                                                                                                                                                                                                                         Genotype-dependent transcriptional activation of novel repetitive elements during cold acclimation of alfalfa (Medicago sativa L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 1732)
Kapila, R., Negi, M.S., This, P., Delseny, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    and Shimamoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4717)
Ivashuta,S., Naumkina,M., Gau,M., Uchiyama,K., Isobe,S., Mizukam,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago sativa
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Theor. Appl. Genet. 930, 1123-1129
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1268. 1732
/note="homology to Bn4 (X67835)"
406 c 339 g 446 t
                                                                                 1586.
                                                                                                  /transposon="LTR retroelement MCIRE"
/note="putative LTR retroelement"
                                                                                                                                         /organism="Medicago sativa"
/db_xref="taxon:3879"
/clone="pMcire7"
/evidence=not_experimental
/product="hypothetical pro
                                                                                                                                                                                                                      Location/Qualifiers
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/db_xref="taxon:3710"
                                        /codon_start=1
                                                         /note="cold-inducible"
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Habitat Place, Lodhi Road, New Delhi,
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                                                                                                                                                                                                                                                               School of Agriculture,
-ku, Sapporo, Hokkaido (
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Best Local Similarity
""" Conserve
Search completed: June 20, 2003, 23:23:59 Job time: 78.956 secs
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Langridge, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Submitted (09-JAN-1992) P. Langridge, University of Adelaide,
Centre for Cereal Blotechnology, Waite Agricultural Res Inst, Glen
Osmond, South Australia 5064, AUSTRALIA
2 (bases 1 to 6676)
2 (bases 1 to 6676)
Rogowsky,P.M., Liu,J.Y., Manning,S., Taylor,C. and Langridge,P.
Structural heterogeneity in the R173 family of rye-specific
                                                                          repetitive DNA sequences
Plant Mol. Biol. 20 (1), 95-102 (1992)
92385773
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Scereale DNA for dispersed repeat sequence (R173-1).
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ERLLSKEEIFEQKGKKVSKAEIDRVIDEICALFKSKLRRTWTSHQLYLKFMEFLPKRR
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/strain="Chinese Spring lBL/lRS, lAL/lRS, lDL/lRS triple
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  Arabidopsis thalia
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Arabidopsis thalia
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Soybean retroeleme
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                                                                                                                                                                                                           Plant retroelement
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					AAZ35254;	AAZ
	BP.	DNA; 18 I		standard;	T 1 254 AAZ35254	SULT 1 Z35254 AAZ
	ALIGNMENTS					
Human bone marrow Probe #8844 for ge Probe #12718 used	AAK38131 AAI18911 AAI44032				14.8 14.8 14.8	444
#9555 brain	ABA63912 ABA31089 AAK12418				444	410
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Human genome-deriv Human cytoskeletal DNA encoding novel	ABS24287 AAS29778 ABK43860				444	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
brain 6 bone ma #17753 #25478	AAK24801 AAK50798 AAI27820 AAI56792		0000	8 8 8 8 8 N N N N	14.8 14.8 14.8	30 31 32
Drosophila melanog Fungal ZBC gene se Plant retroelement Human foetal liver Probe #19153 for g	ABL15328 ABN79856 AAR37624 ABA76135 ABA40687		22236	888888	🗀	25 26 27 28
Stealth virus nucl Human secreted pro Nucleotide sequenc Modified HIV prote Modified HIV prote Modified HIV prote	AAX84348 AAH31356 AAI67895 ABK91610 ABK91615 ABK91608	504057	0000000	& & & & & & & & & & & & & & & & & & &	15.4 15.4 15.4	19 20 21 23 24
Mycobacterium tube Mycobacterium tube Oligonucleotide fo Oligonucleotide fo Fusarium venenatum Human short-chain Novel human secreted pro Drosophila melanog		1529 22 1529 22 1529 24 509 24 778 21 778 21 779 24 770 22 181 23	1 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	855.5.5.5.5 855.5.5.5.5 855.5.5.5 855.5.5 855.5.5 855.	155.4	10 11 12 13 14 14 15 16 16

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28-MAY-1999;
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                                                                                                                                                                                                                                                                                    (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F.
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99US-0087125.
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AA199683

New nucleic acid molecules for imparting agronomically significant

characters

to plants, especially soybean

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RESULT 2
AAZ35271
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX ACA
DT 27-M
XX Retr
KW Caly
OS Glyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
   This is the nucleotide sequence of the Calypso 1-1 retroelement of soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 1 A; 4 C; 9 G; 4 T; 0 other;
                                                                                                                                                                                                                                    New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean -
                                                                                                                                                                                                                                                                                                                              WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                       Wright DA, . Voytas DF
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118pp; English.
                                                                                                                                                                              118pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB
Pred. No. 34;
                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 3
AAZ35275
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     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and retroelement containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least I agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNASe-H sequence (see AAS35254-61). Also provided are plant retroviral particles that contains the sequence selected from the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                           This is the nucleotide sequence of the Calypso 2-2 retroelement of soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and invention provides molecular tools in the form of retroelements
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ35275 standard; DNA; 10482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9829 BP; 2948 A; 2067 C; 2260 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retroelements include gag, sequences that can be used
retroelement-containing vectors, cells and plants. Me provided for introducing the retroelements into cells,
                                                                                                                                                                                                              characters to plants, especially
                                                                                                                                                                                                                                New nucleic acid molecules for imparting
                                                                                                                                                                                                                                                                WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                             Wright DA, Voytas DF
                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calypso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean retroelement Calypso 2-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ35275;
                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                             (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1312 TGGCGCCGTTGTCGGGGA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCCCCTTCTCGGGGA 18
                                                                                                                                                                               Page 107-111; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soybean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retrovirus;
                                                                                                                                                                                                                                                                                                                                 ם ם
                                                                                                                                                                                                                                                                                                                                                                              98US-0087125
99US-0087125
                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US11858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant; gene transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pol, env and primer binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                 soybean
                                                                                                                                                                                                                      agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9829;
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                  Methods are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 4
AAZ35261
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX Reti
XX Reti
XX Reti
XX Soylt
XX WO9:
YM W09:
YM W1:
YM W09:
YM W1:
XX W09:
YM W09:
YM W09:
YM W09:
YM W09:
YM W1:
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YM W1:
XM W09:
YM W1:
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YM W09:
YM W1:
XM W09:
YM W09:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that particles are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WRIG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retroelement; soybean; pea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid
                      retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant
                                                                                               obtained from retrovirus-like elements (retroelements) calypso of soybean, cyclops of pea and athila of Arabidopsis thaliana. The invention provides molecular tools in the form of retroelements and
                                                                                                                                                                                                                                        Claim 1(h); Page 84-88; 118pp; English.
                                                                                                                                                                                                                                                                                          New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-105586/09.
P-PSDB; AAY32434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ35261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ35261 standard; DNA; 12286
                                                                                                                                                                                  The present sequence comprises a generic plant retroelement
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wright DA, Voytas DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant generic retroelement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10482 BP; 3181 A; 1842 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sativum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGCCGTTGTCGGGGA 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retrovirus; transgenic plant; Calypso; athila; cyclops; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D A.
  (ACS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0087125
99US-0087125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1482..6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2297 G;
                                                                                                                                                                                                                                                                                                                      agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene transfer;
a helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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TGGCGCCGTTGTCGGGGA 18

Query Match Best Local Matches

Local Similarity les 17; Conserv

Conservative

0;

Mismatches

Indels Length

0;

Gaps

0

91.1%; 94.4%;

Score 16.4; Pred. No. 1.

.6e+02

DB

21;

687;

Sequence

687

BP;

241 A; 135 C; 115 G; 196 T;

0 other;

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RESULT 5
AAF22107/
88888888x&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2107/c
AAF22107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site.
                                            The present invention relates to a recombinant DNA construct (Arabidopsis thaliana) centromere. The constructs are useful producing stably inherited michrosomes which can serve as vec the construction of transgenic plant and animal cells express the construction of transgenic plant and animal cells express
                                                                                                                                   Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells \cdot
                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12286 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retroviral particles that are used to transfer the nucleic acids into plant cells.
                                    selected
                                                                                                             Claim 108; Page 274; 1449pp; English.
                                                                                                                                                                                                                  Preuss D,
                                                                                                                                                                                                                                                                     17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                   WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centromere; michrosome; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF22107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant
                      factors,
                                                                                                                                                                                                                                            (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1312
                                                                                                                                                                                         2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                     proteins such as hormones, enzymes, interl cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCGCCGTTGTCGGGGA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                 Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana centromere conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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99US-0127409.
99US-0134770.
                                                                                                                                                                                                                                                                     99US-0153584
99US-0154603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3748 A;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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                                  interleukins,
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                                                expressing
                                                            vectors
                                    clotting
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RESULT 7
AAF22303
ID AAF2
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AC AAF2
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AAH51978/
ID AAH5
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                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                    This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an argential as a target for a drug or essential for the growth or viability of
              AAF22303;
                                                                                                                                                                                                                                Sequence 2364 BP;
                                        AAF22303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 71-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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12-NOV-1999;
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DB; AAG81127.
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17; Conserv
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                                                                                                                TGGCGCCGTTGTCGGAGA 1067
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                                                                                                                                                                        Conservative
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99US-0165124.
                                                                                                                                                                                                                                467 A; 775 C; 715 G; 407 T; 0 other;
                                         DNA;
                                                                                                                                                                                    91.1%;
94.4%;
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                                           611590
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                                                                                                                                                                                                   Score 16.4; DB 22;
                                                                                                                                                                                      Pred. No. 1.6e+02;
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RESULT 8
AAI99683
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OS PR XX PR 
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Best Local
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  producing stably inherited michrosomes which can serve as vectors
the construction of transgenic plant and animal cells expressing
selected proteins such as hormones, enzymes, interleukins, clott:
factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                       24-JUN-1998;
                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; strain H37Rv; strain CDC variation; epidemiology; patient treatment; epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI99683 standard; DNA; 4403765 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 611590 BP; 181893 A; 124460 C; 120254 G;
                     24-JUN-1998;
                                                                                                                          25-SEP-2001.
                                                                                                                                                                                                                                  Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis strain H37Rv genome
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 820-959; 1449pp; English.
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                                                                                                                                                                                                                                     tuberculosis
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99US-0134770.
99US-0153584.
                        98US-0103840
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                               genome;
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RESULT 9
AA199683/c
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PT Genome
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4403765
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                                                                        determining the nucleotide genome corresponding to pos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; strain H37Rv; strain CDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variation;
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seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                      and
                                                                                                                                                                                     2001-647261/74
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                                                        H37Rv
                                                                                                                              strain variation of Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidemiology; patient
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                                                                The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
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                                                                                                                                                                                              Evaluating strain variation of Mycobacterium tuberculosis, composite the nucleotide sequence of the strain at positions genome corresponding to positions where M. tuberculosis strains 1551 and H37Rv differ
                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
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                                                                                                                                                                                                                                       Sequence 4411529 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2002 (first entry)
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monitoring; d
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RESULT 12
ABQ35252
ID ABQ35
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                                                                                                            Best Loc
Matches
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                         Sequence 509
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                                                                                                                                                                                                                                                                                   the disclosure of the invention.
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                                                                                                                                         Local
207
                                                                                                                                         Similarity
                                                       GGCGCCGTTGTCGGGGA 18
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                                                                                                         85.6%; Score 15.4; ilarity 94.1%; Pred. No. 4. Conservative 0; Mismatche
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                                                                                                                                                                                                                            A; 63 C; 174 G;
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hybridization
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AC ABQ352
YX 12-JUL
XX Oligon
XX Human;
KW Human;
KW Gastro
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RESULT 14
AAF08402/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CD DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method CI is used: (1) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide CC systems etc., particularly by detecting mutations or single nucleotide CC systems etc., particularly by detecting mutations of cell or tissue CC types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. CR ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the CC methylation of the invention.
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA \, -
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05-SEP-2000;
                            AAF08402 standard; cDNA;
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                                                                                                                                                                                                                                       2 GGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                               Similarity
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2000DE-1044543
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Pred. No. 4
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em; single nucleotide polymorphism;
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                                                                                    Query Match
Best Local
                                                                     Matches
                                                                                                                                                                                        engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 86; Page 737; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \boldsymbol{\cdot}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; Fusarium venenatum; Aspergillus niger Aspergillus oryzae; Trichoderma reesei; identification; recom culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus
                                                                                                                                           Sequence
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                                                                                      Similarity
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                                                                                                                                           ВP;
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                                                                                                                                         184 A;
                                                                                                                                                                             claimed
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                                                                                    85.6%;
94.1%;
                                                                                                                                         232 C; 184 G;
                                                                                                                                                                         in the present invention.
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                                                                                    Score 15.4;
Pred. No. 4.
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                                                                     Mismatches
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                                                                                                                                         176 T;
                                                                                    .7e+02
                                                                                                         DB
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                                                                                                                                           2 other;
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                                                                                                     Length
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                                                                     Gaps
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RESULT 15 ABK87940

ABK87940 standard; cDNA; 1649 BP

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CC The invention discloses an isolated 25206 polypeptide, a human CC short-chain dehydrogenase/reductase (SDR) family member. Members of this CC family catalyse the reversible, rate limiting conversion of retinol to CC retinal. Retinal is then converted to retinolc acid which plays a key CC role in the regulation of embryonic development, spermatogenesis and CC epithelial differentiation. Short chain dehydrogenases are important in CC the metabolism of small molecules, production/removal of biologically CC important molecules that modulate development and growth, elimination of CC conditions. The polynuclectide and polypeptide are useful for identifying CC compounds which binds to them, for identifying compounds which binds to them, for identifying compounds which binds to them, for identifying compounds which modulate CC the activity of the polypeptide in a sample, for modulating aberrant activity of the polypeptide in a sample, for modulating aberrant activity CC of 25206-expressing cells (e.g. a cancerous, pre-cancerous or neural CC aberrant activity. The 25206 molecules can act as diagnostic targets and CC therapeutic agents for controlling one or more cellular proliferative, CC including haematopoietic disorders, or differentiative disorders (e.g. cancer, tumours, carcinoma, sarcoma and Hodgkin's disease, parkinsonism CC and progressive supranuclear palsy) and reproductive disorders (e.g. CC polycystic ovarian disease and ovarian tumours). The sequence presented CC is the human short-chain dehydrogenase/reductase, 25206, cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene; ss; cytostatic; nootropic; neuroprotective; antitumour; 25206; short-chain dehydrogenase; short-chain reductase; SDR; retinol; retinol; retinol acid; embryonic development; spermatogenesis; epithelial differentiation; metabolism; development; growth; proliferative disorder; haematopoletic disorder; cancer; tumour; differentiative disorder; carcinoma; sarcoma; Hodgkin's disease; neurodegenerative disorder; Alzheimer's disease; Parkinsonism; progressive supranuclear palsy; reproductive disorder; ovarian tumours; polyvestic ovarian disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated 25206 polypeptide, a human short-chain dehydrogenase/reductase family member, useful as diagnostic targets and therapeutic agents for treating cancer, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 101-102; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-547697/58.
P-PSDB; AAU99344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-2000; 2000US-250186P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2001; 2001WO-US45040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human short-chain dehydrogenase/reductase, 25206, cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinsonism,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macbeth KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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/*tag= a
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Sequence 1649 BP;

275 A; 543 C; 532 G; 299 T; 0 other;

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                                  Query Match Best Local S
Matches 16
1274 GGCGCCTTTGTCGGGGA 1290
                                  16; Conserv
         2 GGCGCCGTTGTCGGGGA 18
                                   Conservative
                                         85.6%;
94.1%;
                                 Score 15.4; DB 24,
Pred. No. 4.6e+02;
                                                   Length 1649;
                                    Indels
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                                    Gaps
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Search completed: June 20, 2003, 21:58:31 Job time: 22.3019 secs

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Result
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Maximum DB seq
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1: /cgn2_6/ptodata/1/
2: /cgn2_6/ptodata/1/
3: /cgn2_6/ptodata/1/
4: /cgn2_6/ptodata/1/
5: /cgn2_6/ptodata/1/
6: /cgn2_6/ptodata/1/
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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12286
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US-09-452-239-31
US-09-302-620B-94
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US-09-302-620B-94
US-09-302-620B-94
US-09-66-611-29
PCT-US95-05980-14
US-08-661-12-13
US-08-661-12-13
US-08-686-101-3
US-09-086-101-3
US-09-086-101-3
US-09-086-101-3
US-09-199-637h-212
US-09-167-717-3
US-09-231-227-1
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US-09-322-478-39
US-09-322-478-19
US-09-322-478-23
US-09-322-478-17
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                                        Sequence 2, Appli
Sequence 39, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 41, Appli
Sequence 94, Appli
Sequence 94, Appli
Sequence 111, Appli
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Sequence 14, Appli
Sequence 29, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 31, Appli
Sequence 310, Appli
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3322478 iroelements and Methods Plant Retroelement IS/09/322,478 28 50/087125	; Score 18; DB 4; ; Pred. No. 5.8; 0; Mismatches 0; 18	ments and Methods Retroelement 322,478	ALIGNMENTS	US-08-984-709A-52 US-08-356-060A-6 US-08-460-900C-6 US-08-674-509B-6 US-08-957-874-6 US-08-957-874-6 US-08-957-874-6 US-08-958-91-10 US-08-748-591-10 US-08-984-709A-51 US-08-9149-476-123 5248599-1 US-09-129-637A-92 US-09-129-637A-92 US-09-221-017B-225 US-09-221-017B-225
Related Thereto	Length 18; Indels 0; Gaps	Related Thereto		Sequence 52, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 10, Appli Sequence 2, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13, Appli Sequence 123, Appli Sequence 123, Appli Sequence 225, Appli Sequence 32, Appli
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0;

LENGTH: 27
; TYPE: DNA
; ORGANISM: Glycine
US-09-322-478-39

max

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RESULT 5
US-09-322-478-17
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; ORGANISM: Glycine max
US-09-322-478-19
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APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 19
FRACTION 0820
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Matches 18
Sequence 17, Application US/09322478
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                                                                                                                                                 Matches
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Patent No. 6331662
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Best Local :
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Patent No. 6331
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: W19ht, David A.
APPLICANT: W19ht, David F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                              LENGTH: 10482
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18; Conser
                                                                                                                                                                 Similarity
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Pred. No. 4.8;
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Best Local
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APPLICANT: FLEISCHMAN, Robert D.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF THE TOTAL OF THE T
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APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                            FEATURE:
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4130872 TGCCGCCGTTGTCGGGGA 4130889
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                TGGCGCCGTTGTCGGGGA 18
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                                                              Conservative
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94.4%;
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Pred. No. 18;
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RESULT 7
US-09-103-840A-2/c
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 62943208
; Patent No. 62943208
; GENERAL INFORMATION:
CONTROL OF THE PROPERTY DESCRIPTION TO THE PR

APPLICANT: FLEISCHMAN, Robert APPLICANT: WHITE, Owen R.

WHITE,

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US-09-103-840A-1/c
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US-09-103-840A-1
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APPLICANT:
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURPENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                            ENERAL INFORMATION:
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
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CURRENT APPLICATION NUMBER: US/09/103,840A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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17; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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; NAME/KEY: unsure
; LOCATION: (1012)
US-09-452-239-35
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SEQ ID NO 35
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Sequence 35, Approximately No. 6465229
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                                                  Query Match
Best Local :
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Best Local (
                                     Matches
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EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
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CURRENT FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
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TYPE: DNA
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TYPE: DNA
ORGANISM: Triticum
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(970)..(971)
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                                     Conservative
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88.9%;
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Pred. No. 18
                                                 Score 14.8;
Pred. No. 1.
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RESULT 11
US-09-452-239-41/c
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US-09-230-225B-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 3, Application US/09230225B
Patent No. 6403362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Meiji Seika Kaisha, Ltd.
APPLICANT: Moriya, Tatsuki
TITLE OF INVENTION: Systems for the Mass Production of Proteins or
TITLE OF INVENTION: of the Genus Humicola
FILE REFERENCE: VX990054
CURRENT FILING DATE: 1999-03-03
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 34
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EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
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CURRENT FILING DATE: 1999-12-01
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APPLICANT: Fader, Gary M.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Office 97
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TYPE: DNA
ORGANISM: Triticum mestivum
                                                                                                                                                NAME/KEY: Intron
LOCATION: (478)..(535)
OTHER INFORMATION:
                                                                                         LOCATION: (536)..(1029) OTHER INFORMATION:
                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide LOCATION: (458)..() OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                         LOCATION: (458)..(477)
OTHER INFORMATION:
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                                   LOCATION: (1030)..(1141)
OTHER INFORMATION:
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Local Similarity 88.9%;
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 TGGTGCCGTCGTCGGGGA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTGCCGTCGTCGGGGA 440
(1142)..(1761)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09452239
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Pred. No. 1.5e+02;
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                                                                                                                                                ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 3348
; TYPE: DNA
; ORCANISM: Candida tropicalis
US-09-302-620B-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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US-09-302-620B-94
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Best Local Similarity 88.9
16; Conservative
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Patent No. 6331420
                                                                                         Query Match
Best Local
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                                                                          Matches
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/302,620B CURRENT FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 109
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIOCREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 1010-16.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1643)..(1648)
OTHER INFORMATION: Cleavage siteStuI
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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LOCATION: (1505)..(1510)
OTHER INFORMATION: Cleavage site BglII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1253)..(1259)
OTHER INFORMATION: Cleavage site BamHl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (688)..(693)
OTHER INFORMATION: Cleavage site SmaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (2045)..(2095)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1990)..
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Intron
LOCATION: (1762)..(1815)
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OTHER INFORMATION:
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1140 TTGCGCCGTTGTTGGGGA 1157
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                                     1 TGGCGCCGTTGTCGGGGA 18
                                                                        . Similarity
16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang, Maria
Loper, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eirich, Dud.
Eshoo, Mark
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                                                                          Conservative
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88.9%;
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                                                                        Score 14.8; DB 4;
Pred. No. 1.4e+02;
0; Mismatches 2
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Pred. No. 1.4e+02;
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                                                                                                               DB 4;
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; SEQ ID NO 111
; LENGTH: .6909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-611-757-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/199,637A: CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: US 025,396
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Young, LaYonne
TITLE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No. 51
TITLE OF INVENTION: Agents and Molecular Cloning Thereof
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94306
                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                      350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ausubel,
                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reyes, Gregory R. Wages, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Search completed: June 20, 2003, 23:25:44
Job time: 14.1792 secs
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                                                                                                              Matches
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Best Local (
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                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
                                                                                                                                                                                                        MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                      MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICATION NUMBER:
                                                       131 GCGCCGTTGTCGGTGA 146
                                                                      3 GCGCCGTTGTCGGGGA 18
                                                                                                            l Similarity
15; Conserv
                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                              Conservative
                                                                                                                                                                                                                                                 linear
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Pred. No. 2
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                                                                                                            Mismatches
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                                                                                                                                      Length 231;
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Maximum DB seq
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length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna,

2: /cgn2_6/ptodata/2/pubpna,

3: /cgn2_6/ptodata/2/pubbna,
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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'cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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. 0	n .01	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	1.1	1.1				0.0	0.0	Query Match Length
1649	285	276	275	275	273	272	269	269	262	251	2364	2000	12286	10482	9829	27	18	
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sequence 28499, A	Sequence 12806, A	Sequence 8192, Ap				Sequence 11753, A			Sequence 12308, A	ď	Sequence 32, Appl	Sequence 5131, Ap	•	•	Sequence 19, Appl	Sequence 39, Appl	Sequence 2, Appli	Description

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•	US-09-878-574-2125	US-09-878-574-688	US-09-878-574-15351	US-09-878-574-14193	US-09-878-574-10867	US-09-878-574-15236	US-09-878-574-15547	US-09-821-167-8	US-09-738-626-1	US-09-975-719-111	US-09-976-800-94	US-10-138-916-94	US-10-138-905-94	US-10-139-031-94	US-10-138-838-94	US-09-738-626-1258	US-10-121-988-82	US-10-121-988-145	US-10-121-988-79	US-09-452-239-41	US-09-452-239-35	US-09-974-300-5723	US-09-864-761-9555	US-09-918-995-401	us-09-923-876-1817	US-09-864-761-26007
	Sequence 2125, Ap	Sequence 688, App	Sequence 15351, A	Sequence 14193, A	Sequence 10867, A	Sequence 15236, A	Sequence 15547, A	Sequence 8, Appli	Sequence 1, Appli	Sequence 111, App	Sequence 94, Appl	Sequence 1258, Ap	Sequence 82, Appl	Sequence 145, App	Sequence 79, Appl	Sequence 41, Appl	Sequence 35, Appl	Sequence 5723, Ap	Sequence 9555, Ap	Sequence 401, App	Sequence 1817, Ap	Sequence 26007, A				

ALIGNMENTS

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US-09-965-553-39
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Best Local Similarity
Whiches 18; Conserve
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; TYPE: DNA
; ORGANISM: Glycine max
US-09-965-553-2
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US-09-965-553-2
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
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APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel
                                                                                                              Sequence 39, Application US/09965553 Patent No. US20020112259A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn SEQ ID NO 2
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Patent No. US20020112259A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322/478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-05-29
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Pred. No.
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SOFTWARE: PatentIn Ver.
SEQ ID NO 39
LENGTH: 27
TYPE: DNA
ORGANISM: Glycine max
US-09-965-553-39
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; ORGANISM: Glycine max
US-09-965-553-19
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US-09-965-553-19
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                                                                                 Sequence 23, Application US/0996553
patent No. US30020112259A1
GENERAL INFORMATION;
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 60/087125
PRIOR APPLICATION NUMBER: 60/087125
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Patent No. US20020112259A1
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
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Best Local Similarity
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SEQ ID NO 19
LENGTH: 9829
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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                                    PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                     SOFTWARE:
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CURRENT FILING DATE: 2001-09-27
LENGTH: 10482
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; OTHER INFORMATION: Description of Artificial Sequence: plant ; OTHER INFORMATION: retroelement sequence US-09-965-553-17
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US-09-965-553-17
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-842A-5131
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NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5131
LENGTH: 2000
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Best Local (
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Best Local Similarity
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                                                         PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                             PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                      TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                             APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
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PRIOR FILING DATE: 1998-05-29
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APPLICANT: Voyta:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Voytas, Daniel F.
IITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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les 18; Conservative
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Pred. No. 3
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Pred. No.
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ORGANISM: Arabidopsis thaliana

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Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Wocleic Acid Molecules an
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION UNMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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Matches
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SEQ ID NO 32
LENGTH: 2364
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APPLICANT: MATCOTTE, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
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PRIOR FILING DATE: 2000-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/165,086
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RIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                       Local
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FILING DATE: 1999-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/126,593
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5. US20020164588A1
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17; Conser
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Pred. No. 23;
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Pred. No. 2
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PRIOR APPLICATION UNMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 12308
LENGTH: 262
TYPE: DNA
OTHER INFORMATION: Clone ID: 701065609H1
US-09-878-574-12308
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; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 10644

; LENGTH: 251

: TYPE: DNA

: ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 700967905H1

US-09-878-574-10644
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US-09-878-574-12035/c
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Best Local s
Matches 16
                                                                          SEQ ID NO 12035
LENGTH: 269
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TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone
-09-878-574-12035
                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                            TITLE OF INVENTION: Nucleic acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38 8-21(15401)B
CUFRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                APPLICANT: Byrum, Joseph R.
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CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
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                                                                                                              NUMBER OF SEQ ID NOS: 15775
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16; Conserv
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16; Conservative
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Thompson, Michael D
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94.1%;
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94.1%;
                     ID: 701065234H1
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Pred. No. 87;
0; Mismatches
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Pred. No. 8
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APPLICANT: Byrum, Joseph R.
APPLICANY: La Rosa, Thomas J.
APPLICANY: La Rosa, Thomas J.
APPLICANY: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 1091-12-21
PRIOR APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 109333,535
PRIOR APPLICATION NUMBER: US/09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 13422
LENGTH: 269
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701067081H1
US-09-878-574-13422
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US-09-878-574-13422/c
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; Sequence 11753, Application US/09878574
; Patent No. US20020110548A1
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                                                                                                                           TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701064849H1
US-09-878-574-11753
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR ENLING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 11753
LENGTH; 272
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Best Local Similarity
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Patent No. US200201
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Best Local Similarity
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                                                              Local Similarity
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 GGCGCCGTTGTCGGTGA 210
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                                                                  Conservative
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94.1%;
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Pred. No. 8
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Pred. No. 8
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Pred. No. 8
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE OF INVENTION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
FRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID MOS: 15775
SEQ ID NO 12670
LENGTH: 275
LENGTH: 275
TYPE: DNA
ORGANISM: Glycine max
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID:
US-09-878-574-15624
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US-09-878-574-15624/c
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US-09-878-574-12670/c
                                                                                                              US-09-878-574-14365/c
; Sequence 14365, Application US/09878574
; Patent No. US20020110548A1
                                                                                                                                                                               RESULT 15
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LENGTH: 273
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APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14
                                                                                          GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael |
TITLE OF INVENTION: Nucleic Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y Match 85.6%;
Local Similarity 94.1%;
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94.1%;
      acid Molecules and
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Pred. No. 8
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 6	u	c 4	ω	2	c 1	Result
18	18	18	18	18	18	sult No. Score
100.0	100.0	100.0	100.0	100.0		Query
690	678	668	624	552	250	Length DB
17	17	17	17	17	17	. 60
BH484542	BH214458	вн600565	BH545031	BH731480	AQ288973	ID
				BH731480 BOHZO16TF	AQ288973 nbxb0033H	Description

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441 443 444 5	333333333333333333333333333333333333333	12222222222222222222222222222222222222	110 110 110 110 110 110 110 110
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BH705588 BH745888 BH514295 BH557816 BH700667 BH727785	BE086799 AW679402 BH650606 AZ92212 BH501549 AZ92219 BC00XJK BH430253 BH744134	BH 7 / 24 8 3 1 BH 5 1 4 3 6 BH 5 3 1 9 3 2 BH 4 2 0 8 3 5 BH 4 5 4 3 5 0 BF 6 2 0 5 0 1 BF 6 2 0 5 0 1 BH 5 1 4 6 9 BH 6 9 8 1 4 9	BH725980 BI642756 BH552125 BH441346 BH424623 BH141140 BH505910 BH505910 BH50633 BH423648 BH700732
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BOHVH74TF 9z73e08.b BOGJQ18TF BOGXT09TF BOMHQ22TF BOHZK26TF			

ALIGNMENTS

FEATURES Source				COMMENT	JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AQ288973/c
Location/Qualifiers 1. 250	EMAII: TWINGECIEMSON.EQU Seq primer: TAATACGACTCACTATAGGG Class: BAC ends High quality sequence stop: 117.	Tel: 864 656 4293	Clemson University Genomics Institute Clemson University 100 Tordan uall Clemson SC 20634 HSA	Contact: Wing RA	Unpublished (1998)	Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Rice Genome	1 (bases 1 to 250)	Ehrhartoideae; Oryzeae; Oryza.	<pre>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;</pre>	Oryza sativa	Oryza sativa.	GSS.	AQ288973.1 GI:3950419	AQ288973	nbxb0033H14f CUGI Rice BAC Library Oryza sativa genomic clone	AQ288973 250 bp DNA linear GSS 03-DEC-1998	

/cultivar="Nipponbare" ∕organism="Oryza sativa"

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RESULT 2
BH731480
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AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 552)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome.shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHZO16TR
                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH731480 552
BOHZO16TF BO_2_3_KB Brassica
                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica oleracea.
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/db_xref="taxon:3712"
/clone="BOHZO16"
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
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                                                                      /organism="Brassica oleracea"
/strain="TO1000DH3"
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Pred. No. 2e+02;
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BH600565
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BH545031
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9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Town.C.D., Van Aken.S., Utterback.T. and Fraser.C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGCW07TR
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Brassica oleracea
Eukaryota; Viridi
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Class: sheared ends.
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                         Brassica oleracea.
                                                      вн600565.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
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301-838-0208
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                                                                                                                                                                                                                                                                                                       /clone_lib="BOGC"
/note="Vector: pHOS1; Site
/note="Vector: pHOS1; Site
genomic DNA inserted into
129 c 109 g 201
                                                                                              BOGD
                                                                                                                                                                                                                                                                                                                                                            /organism="Brassica oleracea"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BOGCW07"
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Viridiplantae;
                                                       GI:17853011
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Pred. No. 2.5e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                    Score 18; DB 17;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                       Mismatches
                                                                                                           dd 899
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19 BStXI
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RESULT 5
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                                                                                                                                                                                                          Agronomy Department
IOWA State University
Ames, IA 50011-1010, USA
Tel: 515 294 1205
Fax: 515 294 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 TGGCGCCGTTGTCGGGGA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GM_UMD001_098_A01_F UMN Soybean BAC Library (pECSBAC4 ECORI) Glycine max genomic clone Glycine max genomic clone GM_UMb001_098_A01, DNA sequence.

BH214458
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSS: BOGDG03TF
                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Shoemaker Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conser
Seq primer: M13F
Class: BAC ends.
                                    see as an authority for the mapping/naming: Cregan P.B., T. Jarv A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. VanToai, D.G. Lohnes, J. Chung, and J.E.Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490.
                                                                                                                                                                                                                                                                                                                                        Marek, L.F., Paz, M., Darnielle, L., BAC End sequences from a soybean
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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DNA is from a doubled haploid provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris Town
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                                                                                                                                http://genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase.
                                                                                                                                                                    Email: rcsshoe@iastate.edu
This BAC identified by SSR Satt077.For more information, see
                                                                                                                                                        SoyBase at:
                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 678)
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/note="Vector: pHOS1; Site_1: BstxI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
146 c 144 g 192 t
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1. .668
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/clone="BOGDG03"
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/strain="TO1000DH3"
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. 2.7e+02;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Tel: 301-838-3523 Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOGWE45TR
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1 (bases 1 to 690)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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Brassica oleracea
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BOGWE45TF BOGW Brassica
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100.0%; ilarity 100.0%; Conservative
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/tissue_type="cotyledon leaves"
/dev_stage="cotyledon"
                                                                                                                                      /clone_lib="BOGW"
/clone_lib="BOGW"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; BstXI; 2-3 kb sheared
/note: pHOS2; BstXI; 2-3 kb sheared
/note: pHOS2; BstXI; 2-3 kb sheared
/n
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/db_xref="taxon:3847"
/clone="Gm_UMb001_098_A01"
                                                                                                                                                                                                                                                                                                                                                     /organism="Brassica oleracea"
/strain="TO1000DH3"
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Score 18; DE
Pred. No. 2.7
0; Mismatches
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Pred. No. 2.7e+02;
; Mismatches 0;
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DB 17;
2.7e+02;
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                                                        Length 690;
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RESULT 7
BH725980
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BI642756/c
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AUTHORS
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ORGANISM
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Best Local S
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BOMMT13TR BO_2_3_KB Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOMMT13TF Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea
Brassica oleracea
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                                                                                                                                                              EST.

Robinia pseudoacacia.

Robinia pseudoacacia

Robinia pseudoacacia

Robinia pseudoacacia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papillonoideae; Robinieae;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Robinieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BI642756 697 bp mRNA linear EST TZS973 TZS (Sapwood-heartwood transition zone of black Summer) Robinia pseudoacacia cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid
Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Kamdem, D.P. and Keathley, D.E.
Analysis of gene expression patterns in trunk wood black locust (Robinia pseudoacacia)
                                                                                                                                                                                                                                                                                                                                                                                                                BI642756
                                                                                                                                                                                                                                                                                                                                                                               BI642756.1 GI:15544966
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                                                                                                                          (bases 1 to 697)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon;3712"
/clone="BOMMT13"
/clone="BOMMT13"
/clone=1b="BO_2_3_KB"
/clone=1b="BO_2_3_KB"
/clone=1b="BO_2_3_KB"
/clone=1b="BO_2_3_KB"
/clone=1bOMMT13"
/clone=1bOMMT13
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1. .694
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/strain-"TO1000DH3"
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Pred. No.
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                                              of a mature
                                                                                                             Retzel, E.F.,
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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BH552125
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Query Match
Best Local Similarity
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Contact: Kyung-Hwan Han
Content of Forestry
Department of Forestry
Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
BH552125
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Fax: 517 432 1143
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                                                                                                                                                                                                                                                                                                                         Town,C.D., Van Aken,S.,
Whole genome shotgun seq
Unpublished (2001)
Other_GSSs: BOHES25TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH552125
BOHES25TF BOHE Brassica
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вн552125.1
                                                                                                                                                                                                           Email: cdtown@tigr.org
DNA is from a doubled haploid provided
Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea.
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                                                                                                                                                                                                                                                                                                               Contact: Chris Town
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                                                                                                                                                                                                                                                        Medical Center Drive,
301-838-3523
301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hanky@msu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /.uote="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi IB; The cDNA library was made from the sapwood-heartwood transition zone of a mature black locust tree collected in Michigan in late July."

Michigan in late July."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_lib="TZS (Sapwood-heartwood transition zone black locust - Summer)"
                                                                                                              /organism="Brassica Ole
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHES25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="sapwood-heartwood/dev_stage="mature tree"/note="Vector: lambda TriplEx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                       /note="Vector: pHOS1; Site_1: BstXI; genomic DNA inserted into pHOS1 using 181 c 138 g 198 t
                                                                                                                                                                       Location/Qualifiers
1. .708
                                                                                                 /clone_lib="BOHE"
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    100.0%;
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sequencing of Brassica oleracea
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     Score 18;
Pred. No.
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genomic
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2.7e+02;
       ; DB 17;
. 2.7e+02;
                                                             pHOS1 using
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                    Length 708;
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g BstXI linkers"
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BOHES25, DNA
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KEYWORDS
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BH445346
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AUTHORS
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       COMMENT
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                                                                               Brassica oleracea.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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BH424623
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BOGEE39TR BOGE Brassica
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHNP83TF
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GSS.
                     Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                         1 (bases 1 to 722)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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/note="Vector: pHOS1; Site_1: BstxI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
179 c 135 g 202 t
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/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BOHNP83"
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Pred. No. 2.7e+02;
Pred. No. 2.7e+02;
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                                                                                                                                                                        Sequence on contig Gm_A455_ctg_a near unmapped duplicate of pA455. For more information, see SoyBase at:

http://genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase&class=Locus. Please see as an authority for the mapping/naming: Cregan P.B., T. Jarvik, A.L. ush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. VanToai, D.G. Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490
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Fax: 612 625 9728
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Pathology University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Young Nevin D
                                                                                                                                                                                                                                                                                                                                                                                                                                       Larsen, D., Mudge, J., De
BAC end sequences from
Unpublished (2001)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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DNA is from a doubled haploid
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                    Email: neviny@tc.umn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Clone="BOGEE39"
/Clone_lib="BOGE"
/clone_lib="BOGE"
/clone_lib="BOGE"
/clone_lib="BOGE"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1, Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
a 132 c 110 g 226 t
/db_xref="taxon:3847"
/clone_lib="UMN Soybean BAC Library (pECSBAC4 EcoRI)
Glycine max genomic clone"
/tissue_type="cotyledon leaves"
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/strain="TO1000DH3"
                                                                                           /organism="Glycine max"
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2.7e+02;
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AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 747)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGDT64TF
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Fax: 301-838-0208
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BH590633
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                                                                                                                                                                                                                        /clone_lib="BOGD"
/clone_lib="BOGD"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
188 c 136 g 209 t
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/strain="TO1000DH3"
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/clone="BOGDT64"
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Other_GSSs: BOHBZ5ZTR
Contact: Chris Town
TIGR
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1 (bases 1 to 768)

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                          Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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DNA is from a doubled haploid
                 Class: sheared ends.
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                                                              cdtown@tigr.org
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" a 169 c 179 g 213 t
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/clone="BOHBZ52"
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